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Sequence 9, Appli
Sequence 9, Appli
Sequence 4091, Ap
Sequence 1186, Ap
Sequence 13778, A Sequence 46, Appl
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8901.834 Million cell updates/sec
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                                                                                  May 27, 2005, 20:17:15 ; Search time 268 Seconds
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(cgn2_6/ptodata/1/ina/6A_COMB.seq:*

(cgn2_6/ptodata/1/ina/6B_COMB.seq:*

(cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

(cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-641-638-46

US-10-170-097-49

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US-09-949-016-15833

US-09-949-016-15833

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US-09-907-794A-376
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US-09-905-125A-376 US-09-902-775A-376	US-09-906-100-376	US-09-903-603A-376	US-09-904-920A-376	US-09-909-064-376	US-09-905-381A-376	US-09-906-618-376	US-09-535-521-10	US-09-535-521-12	US-09-535-521-13	US-09-535-521-15	US-09-535-521-16	US-09-535-521-18	US-09-535-521-19	US-09-535-521-21	US-09-535-521-4	US-09-535-521-6
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ALIGNMENTS

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US-09-111-470-3
Sequence 3, Application US/09111470
Patent No. 6277959
GENERAL INFORMATION:
APPLICANT: Ravel, Odile
APPLICANT: Ravel, Odile
APPLICANT: Ravel, Odile
APPLICANT: Ravel, Odile
APPLICANT: Ravel, John
APPLICANT: Bates, Elizabeth E.M.
APPLICANT: Lebecque, Serge J.E.
TITLE OF INVENTION: Mammalian Membrane Protein Genes;
ITTLE OF INVENTION: Mammalian Membrane Protein Genes;
ITTLE OF INVENTION: Melated Reagents
NUMBER OF INVENTION: Melated Reagents
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSER: DNAX Research Institute
STRET: 901 California Avenue
STRET: 910 California Avenue
CONNTRY: USA
ZIP: 94304-1104
ZIP: 94304-1104
STREE: California
CONNTRY: IMP Compatible
COMPUTER: IMP Compatible
COMPUTER: IMP Compatible
COMPUTER: INP COMPUTER: INP (90-JUL-1999
STREE: PLING DATE: 00-JUL-1999
STRING DATE: 00-JUL-1997
APPLICATION NUMBER: US 60/053,080
FILING DATE: 00-JUL-1997
ATTORNEY CATION NUMBER: US 60/053,080
FILING DATE: 00-JUL-1997
ATTORNEY CATION NUMBER: 130
SEGISTRATION NUMBER: 130
SEGISTRATION NUMBER: 1400
STELECOMPUTION TON REPORMATION:
FELENCHONE CHARACTERISTICS:
LENCYTH: 1458 Dase pairs
TELECOMPUTION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENCYTH: 1458 Dase pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: NUMBER: CDN
FERTINGE TYPE: CDN
FERTINGE
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APPLICANT: Valladeau, Jenny
APPLICANT: Ravel, Odile
APPLICANT: Ravel, Odile
APPLICANT: Ravel, Odile
APPLICANT: Ravel, Odile
APPLICANT: Facts, Ilizabeth Ester Mary
APPLICANT: Ford, John
APPLICANT: Lebecque, Serge J.E.
APPLICANT: Saeland, Sem
TITLB OF INVERTION: Isolated Mammalian Membrane Protein Genes; Related Reagents
FILE REFERENCE: SF0695 B
CURRENT APPLICATION NUMBER: US 60/053,080
FILING APPLICATION NUMBER: US 60/053,080
FRIOR FILING DATE: 1998-07-08
FRIOR FILING DATE: 1998-07-08
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 1458
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Patent No. 6756478
GENERAL INFORMATION:
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NAME/KEY: misc_feature
LOCATION: 608
LOCATION: 608
LOCATION: 608
COTHER INFORMATION: nucleotides 608-673"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 775
OTHER INFORMATION: /note= "ASGPRm (table 2) has
OTHER INFORMATION: sequence insert encoding GEB between nucleotides 775-776"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1064
LOCATION: 1064
OTHER INFORMATION: /note= "nucleotide 1064 of DCMP28
OTHER INFORMATION: may be A, which would encode asn rather than asp at the recorder in the recorder of the code and rather than app and the recorder in the recorder i
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Best Local Similarity 100.
Matches 1458; Conservative
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43 <i>&</i> 3	음 장 1	8 8 1	8 & 8	& 8	አ	8 8	රි සි	& g	රු සි	ර් සි	ර් යි	& A	RE US			** ** ** ** **
; TYPE: DNA ; ORGANISM: Unknown ; FEATURE: ; OTHER INFORMATION: mammalian nucleic acid and protein ; FEATURE:				; NAME/KEY: misc_feature ; LOCATION: (1064)(1064) ; OTHER INFORMATION: nucleotide 1064 of DCMP2s may be A, which would encode Asn rather ; OTHER INFORMATION: than Asp at the residue numbered 270 US-09-862-8028-3		ATGGGATGTC ATGGGATGTC	Qy 61 AGGACTCCAGCTCTCACCCCAGCTCTCCAGGACACACGAGCTCCCAACTCTGAGTGAC 120 Db 61 AGGACTCCAGCTCCTACCCCAGCTCTCCAGGACACAGCGCTCCCAACTCTGAGTGAC 120	Qy 121 GTCCCACCTCTGGTCCTTGCAGCAAACCAACGTGGGAATCACCCTCCAGACCTCCA 180 121 GTCCCACCTCTGGTGGAACCAAACCAAACGAATCACACCTCCAAACCTCCCAAACCAAACCAAACCAAACCTCCAAACCTCCCAAACCTCCCAAACCAAACCAAACCAAACCAAACCAAACAAACAAACAAACAAACAAACAAAA	Qy 181 CAGCTCCACCCCAGACTGGGCCCCGGCCCTGCCTTTCAGCTGTGACCACCTCAGAG 240 Db 181 CAGCTCCACCAGACTGGGCCCTGCCTGCCTCCATTCAGCTGTGACACCTCAGAG 240	Qy 241 CCGTGTTGGCCCAAGCATGACAAGGACGTATGAAAACTTCCAGTACTTGGAGAATAAGGT 300 Db 241 CCGTGTTGGCCCAAGCATGACAAGGACGTATGAAAACTTCCAGTACTAGAGAATAAGGT 300	Qy 301 GAAAGTCCAGGGGTTTAAAAATGGGCCACTTCCTCTCCAGTCCTCCTGCAGGTCTCCG 360 11	Qy 361 CTCTGGGCCTGCCATCTCCTGCTGCTCGCCTGCTGCTGCTGCTGCTGGTCATCAT 420 Db 361 CTCTGGGCCTGCCATCTCCTGCTGTCCCTGGGCCTGCTGCTGCTGGTCATCAT 420	Qy 421 CTGTGTGGTTGGATTCCAAATTCCAAATTTCAGAGGGCCTGGTGACCTGGAACAGA 480	Oy 481 ITTTAGCAACTTCACCTCAAACACTGGGGGGGAGATCCAGGCACTGACTTCCCAGGGCAG 540 LIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 541 CAGCTTGGAAGAAACGATGGCATCTCTGAAAGCTGAGGTGGAGGGTTTCAAGCAGGAACG 600 	Oy 601 GCAGGCAGGGTATCTGAGCTCCAGGAACACACTACGCAGAAGGCACCCTAGGCCACTG 660

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467 GGCGGAGATCCAGGCACTGACTTCCCAGGGCAGCAGCTTGGAAGAAACGATAGCATCTCT 526
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                                  GAAAGCTGAGGTGGAGGGTTTCAAGCAGGAACGGCAGGGCAGGGGTATCTGAGCTCCAGGA
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Patent No. 6756478
GENERAL INFORMATION:
APPLICANT: Ravel, Jenny
APPLICANT: Ravel, Odile
APPLICANT: Fares, Elizabeth Ester Max
APPLICANT: Ford, John
APPLICANT: Lebecque, Serge J.E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1370;
                                                                             COMPUTER KEALABLE FORM:

MEDIUM TYPE: FIDOPP disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM:
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/111,470
FILING DATE: 08-JUL-1998
CLASSIFICATION NUMBER: US 60/053,080
FILING DATE: 09-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAMME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: SF0695
TELEPHONE: (650)496-1200
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTER/STICS:
LENGTH: 1370 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 76.0%; Score 1108; DB 3; Sest Local Similarity 89.4%; Pred. No. 2.7e-288; Matches 1288; Conservative 0; Mismatches 5;
                                               ZIP: 94304-1104
COMPUTER READABLE FORM:
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273..1091
                 California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY:
; LOCATION:
US-09-111-470-9
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Sequence 4091, Application US/09949016

Sequence 401, Application US/09949016

Sequence 401, Application US/09949016

Jakent No. 6812339

Tare No. 6812339

TITLE OF INVENTION: POLYMORHIEMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TILE REFERENCE: CL001307

CURRENT APPLICATION WYBER: 08/09/949,016

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 1224

TYPE: DNA
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       566 AGTTCATTCTGAAATGCTCCTGCGAGTCCAGCAGCTGGTGCAAGACCTGAAGAAACTGAC 625
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                                         CTGCCAGGTGGCTACTCTCAACAAT------GCCTCCACTGAAGGGACC
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APPLICANT: Saeland, Sem
TITLE OF INVENTION: Isolated Mammalian Membrane Protein Genes; Related Reagents
TITLE OF INVENTION: Isolated Mammalian Membrane Protein Genes; Related Reagents
TILE REFERENCE: $80638
CURRENT APPLICATION NUMBER: US/09/862,802A
CURRENT FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/053,080
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1998-07-06
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 1370
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                                                                                                                                                                                                                                                                                             OTHER INFORMATION: mammalian nucleic acid and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                2,
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

76.0%; Score 1108; DB 4;
Best Local Similarity 89.4%; Pred. No. 2.7e-288;
Matches 1288; Conservative 0; Mismatches 5;
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1 LOCATION: (273)..(1091)
2 OTHER INFORMATION: protein coding sequence
US-09-862-802A-9
                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Unknown
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                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Sellhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           284 TACTIGGAGAATAAGGIGAAAGICCAG---GGGITTAAAAAAIGGGCCACTICCI
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Word Perfect 6.1 for Windows/MS-DOS 6.2
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66.1%; Pred. No. 1.3e-92;
iive 0; Mismatches 245;
                                                                                                                                                                                                                                                                                                                       ADDRESSEE: INCYTE PHARMACEUTICALS, INC. STREET: 3174 PORTER DRIVE CITY: PALO ALTO STATE: CALIFORNIA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REPERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPRAX: (650) 845-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1186:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/09/016,434
                                                                                                                ; Sequence 1186, Application US/09016434
; Patent No. 6500938
  1016 GACAAGGCCAGCCAGGAG 1033
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Flogby disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1277 base pairs
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APPLICATION NUMBER: US
FILING DATE: HEREWITH
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STRANDEDNESS: single
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US-09-016-434-1186
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                                                                     RESULT 6
US-09-016-434-1186
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                                                                                                                                                                                                                                                    284 TACTIGGAGAATAAGGIGAAAGICCAG---GGGITIAAAAAIGGGCCACTICCICICCAG 340
                                                                                                                                                                                                                                                                              341 TCCCTCCTGCAGCGTCTCCGCTCTGGGCCCTGCCATCTCCTGCTGTCCCTGGGCCTTCGC 400
                                                                                                                                                                                                                                                                                                                                                                       260 CCCTCCTGCAGCGTCTCTGCTCCGGACCTCGCTCCTCCTCCTCCCTGGGCCTCAGC 319
                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGCTGCTGCTGGTCATCATCTGTGGTTGGATTCCAAAATTCCAAATTTCAGAGGAC 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGGTGACCCTGAGAACAGATTTTAGCAACTTCACCTCAAACACTGTGGCGGAGATCCAG 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCACTGACTTCCCAGGGCAGCTTGGAAGAACGATAGCATCTCTGAAAGCTGAGGTG 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         440 GGCTTGAGCACCCAGGGAGGCAATGTGGGAAGAAGAAGATGAAGTCGCTAGAGTCCCAGCTG 499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              599 GCGCTCCAGGGCAATGGCT---CAGAAAGGACCTGCTGCCCGGTCAACTGGGTGGAGCAC 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            821 CAAGACAGCTGCTACTGGTTCTCTCACTCTGGGATGTCCTGGGCCGAGGCTGAGAAGTAC 880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          715
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                                                                                                                                                           224 CTGTGACAACCTCAGAGCCGTGTTGGCCCAAGCATGACAAGGACGTATGAAAACTTTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  500 GAGAAACAGCAGAAGGACCTGAGTG---------
                                                                                                                   Gaps
                                                                                                              87;
                                                                     Length 1224;
                                                                   Score 382; DB 4; Length 12
Pred. No. 1.3e-92;
0; Mismatches 245; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1181 GGTCAGACCAGCCAGGAG 1198
                                                                Query Match 26.2%;
Best Local Similarity 66.1%;
Matches 646; Conservative
ORGANISM: Human
    ; ORGANISM: HUMA
US-09-949-016-4091
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US-09-949-016-4090

Sequence 4090, Application US/09949016

Patent No. 6812339

GENERAL INPORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PLICATION NUMBER: 60/237,768

PRIOR PLICATION NUMBER: 60/237,768

PRIOR PLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FREESEQ for Windows Version 4.0

LEMOTH: 1348

LEMOTH: 1348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTCCCACTCTGGACCACAACCAACGTGGGAATCACACCTCCAGACCTCCCA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 GTTGAGGAGATGGGATGKSCCAGAKGATAGGGCTCCTGGGATTTCAGACCCAAGACCAGC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 CCGTGTTGGCCCAAGCATGACAAGGACGTATGAAAACTTCCAGTACTTGGAGAATAAGGT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            290 CCGTGTTGGCCCCAAGCATGACAAGGACGTATGAAAACTTCCAGTACTTGGAGAATAAGGT 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           170 Greccacereregreceriscascascas carcas careacas careacereces con 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            230 caccreceaceceasacresses ceseceres erecentes are respected as a caccrea can can be seen as a caccrea can be seen as a caccrea can be seen as a caccrea cacac ca
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Pred. No. 2.8e-65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 310.4; DB 4; Length 361;
Pred. No. 1.3e-73;
4; Mismatches 0; Indels 0
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61.4%;
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Best Local Similarity 98.7%;
Matches 308; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 74
OTHER INFORMATION: k=g or t
FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: 136 -
; OTHER INFORMATION: y=c or t
US-09-513-999C-13778
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                                        LOCATION: 67

LOCATION: 67

FEATURE: INFORMATION: k=g or FEATURE: misc_feature
LOCATION: 68

OTHER INFORMATION: 8=g or FEATURE:
NAME/KEY: misc_feature
          NAME/KEY: misc_feature
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Best Local Similarity
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ORGANISM: Human
-09-949-016-4090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGAAATATCTAGGCTCCGCATACACCTGGATGGGCCTCAGTGACCCTGAAGGAGCCTGG 1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           599 GCGCTCCAGGGCAATGGCT---CAGAAAGGACCTGCCCGGTCAACTGGGTGGAGCAC 655
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                                                                                                                                                                                                                                                                                           GAGGGTTTCAAGCAGGAACGGCAGGCAGGGGTATCTGAGCTCCAGGAACACACTACGCAG 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----AAGATCACTCCAGC 538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             821 CAAGACAGCTGCTACTGGTTCTCTCTGGGATGTCCTGGGCCGAGGCTGAGAAGTAC 880
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                                                                                                GCACTGACTTCCCAGGGCAGCTTGGAAGAAACGATAGCATCTCTGAAAGCTGAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             761 ACTCTCAACAACAATGCCTCCACTGAAGGGACCTGCTGCCCCGTCAACTGGGTGGAGCAC
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Patent No. 6783961

GENERAL INFORMATION:

APPLICANT: Dumas Mine Edwards, J.B.

APPLICANT: Dumas Mine Edwards, J.B.

APPLICANT: Glordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

PATENT G193961

FILE REFERENCE: 59.US2.REG

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT PILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/122,487
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SOFTWARE: Patent.pm
SEQ ID NO 13778
LENGTH: 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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ATTLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
FILE REFERENCE: GENSET.051CP1
(CURRENT APPLICATION NUMBER: US 09/641,638
CURRENT FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 1999-05-07
PRIOR FILING DATE: 1999-05-12
NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-02-12
NUMBER: PRIOR PRIOR FILING DATE: 1999-02-12
SEQ ID NO 46
LENGTH: 400
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NAME/KEY: misc_binding
LOCATION: 129..148
LOCATION: 129..148
LOCATION: 129..148
LOCATION: 120..148
LOCATION: 1.20
LOCATION: 1.20
LOCATION: 1.20
LOCATION: 1.20
LOCATION: 380..400
COTHER INFORMATION: downstream amplification primer
NAME/KEY: primer bind
LOCATION: 380..400
COTHER INFORMATION: 12-198-128 potential probe
LOCATION: 116..140
COTHER INFORMATION: 12-198-128 potential probe
LOCATION: 12-198-128 potential probe
LOCATION: 12-198-128 potential probe
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LOCATION: 128
COTHER INFORMATION: 12-198-128 : polymorphic base A or G
NAME/KEY: misc_binding
LOCATION: 108..127
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 Bougueleret, Lydie
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Best Local Similarity 98.9
Matches 183; Conservative
                   Chumakov, Ilya
Cohen, Annick
                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo Sapiens
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                                                        259 GAGGAAATCCATTTTTGAAAGGCAAGGCACCTCCTGCCCAGCCCCTGGCACAGCGTCT 318
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                                   299 GTGAAAGTCCAGGGGTTTAAAAATGGGCCACTTCCTCTCCAGTCCCTCCTGCAGCGTCTC
                                                                                                           359 CGCTCTGGCCCTGCCATCTCCTGCTGTCCCTGGGCCTCGGCCTGCTGCTGCTGGTCATC
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0; Mismatches 254; Indels
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562; Conservative
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APPLICANT: Blumenfeld, Marta

Sequence 46, Application US/09641638; Patenn No. 6432648; Patenn No. 6432648; APPLICANT: Blumenfeld, Marta

Bougueleret, Lydie

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LOCATION: 429..448
OTHER INFORMATION: downstream amplification primer, complement
NAME/KEY: misc binding
LOCATION: 117..141
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LOCATION: 130.149
OTHER INFORMATION: 12-214-129.mis2, potential complement
NAME/KEY: primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: allele
LOCATION: 129
OTHER INFORMATION: 12-214-129 : polymorphic base C or T
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OTHER INFORMATION: upstream amplification primer
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; OTHER INFORMATION: 12-214-129 potential probe
US-09-641-638-49
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                                                                                                                    Sequence 49, Application US/09641638
Patent No. 6432648
GENERAL INFORMATION:
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LOCATION: 110._128
OTHER INFORMATION: 12-214-129.mis1
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ORGANISM: Homo Sapiens
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US-10-170-097-49
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APPLICANT: BOUGUELEIEL, LYLEA
APPLICANT: Chumakov, IJya
APPLICANT: Chumakov, IJya
APPLICANT: Chumakov, IJya
APPLICANT: Chen, Annick
ITILE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
ITILE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
FILE REFERENCE: GEN-T114XC2D1
CURRENT FILING DATE: 2002-06-10
CURRENT APPLICATION NUMBER: US 09/641,638
PRIOR FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 1999-05-07
PRIOR FILING DATE: 1999-05-07
PRIOR FILING DATE: 1999-03-21
PRIOR FILING DATE: 1999-03-22
PRIOR FILING DATE: 1999-03-22
PRIOR FILING DATE: 1999-03-21
SPRIOR APPLICATION NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-03-21
SPRIOR PRIOR PRIOR PRIOR PRIOR PRIOR FILING DATE: 1999-03-21
SPRIOR PRIOR PRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: primer bind
LOCATION: 380..400
OTHER INFORMATION: downstream amplification primer, complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 12.6%; Score 183; DB 4; Length 400; Best Local Similarity 98.9%; Pred. No. 3.1e-39; Matches 183; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_binding
LOCATION: 129._148
JTHER INFORMATION: 12-198-128.mis2, potential complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 128
OTHER INFORMATION: 12-198-128 : polymorphic base A or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1..20 -
OTHER INFORMATION: upstream amplification primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 108.7127
OTHER INFORMATION: 12-198-128.mis1, potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 116.7140
OTHER INFORMATION: 12-198-128 potential probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: 249 7; COTHER INFORMATION: n=a, g, c or t
US-10-170-097-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo Sapiens
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NAME/KEY: primer_bind
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: allele
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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| GENERAL INFURMATION:
| APPLICANT: Blumenfeld, Marta |
| APPLICANT: Blumenfeld, Marta |
| APPLICANT: Blumenfeld, Marta |
| APPLICANT: Chumakov, Ilya |
| APPLICANT: Chen, Annick |
| TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM |
| TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM |
| TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM |
| CURRENT APPLICATION NUMBER: US 09/502,330 |
| PRIOR APPLICATION NUMBER: US 60/133,200 |
| PRIOR FILING DATE: 1999-03-23 |
| PRIOR FILING DATE: 1999-03-23 |
| PRIOR FILING DATE: 1999-03-21 |
| NUMBER OF SEQ ID NOS: 1304 |
| SOFTWARE: Patent.pm |
| SEG ID NO 49 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    835
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 TGGTTCTCTCACTCTGGGATGTCCTGGGCCGAGGCTGAGAAGTACTGCCAGCTGAAGAAC 222
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RESULT 14
US-09-641-638-571
Sequence 571, Application US/09641638
Patent No. 6432648
Blumenfeld, Marta
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ORGANISM: Homo Sapiens
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                      APPLICANT: BOUGUELETE, LYdie
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chen, Annick
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC RECIONS
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
FILE REPERENCE: GEN-TITACZOU
FILE REPERENCE: GEN-TITACZOU
CURRENT APPLICATION NUMBER: US/10/170,097
CURRENT FILING DATE: 2000-06-10
FRIOR PELICATION NUMBER: US 09/502,330
FRIOR FILING DATE: 2000-02-11
FRIOR PELICATION NUMBER: US 60/133,200
FRIOR FILING DATE: 1999-06-07
FRIOR FILING DATE: 1999-03-23
FRIOR FILING DATE: 1999-02-12
FRIOR FILING DATE: 1999-03-23
FRIOR FILING DATE: 1990-03-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             836 TGGTTCTCTCACTCTGGGATGTCCTGGGCCGAGGCTGAGAAGTACTGCCAGCTGAAGAAC 895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 10.7%; Score 155.6; DB 4; Length 448; Best Local Similarity 99.4%; Pred. No. 8e-32; Matches 155; Conservative 1; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 130.7149 OTHER INFORMATION: 12-214-129.mis2, potential complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: 12-214-129 : polymorphic base C or T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           896 GCCCACCTGGTGGTCATCAACTCCAGGGAGGAGCAG 931
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; OTHER INFORMATION: 12-214-129 potential probe
US-10-170-097-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
US-09-641-638-51
Sequence 51, Application US/09641638
Patent No. 6432648
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: misc_binding
LOCATION: 110..128
OTHER INFORMATION: 12-214-129.misl
APPLICANT: Blumenfeld, Marta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_binding
LOCATION: 117..141
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ORGANISM: Homo Sapiens
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NAME/KEY: primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: allele
LOCATION: 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 448
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APPLICANT: BOUGHELECT, LYdie
APPLICANT: Chumakov, 11ya
APPLICANT: Chumakov, 11ya
APPLICANT: Chumakov, 11ya
APPLICANT: Chen, Annick
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
FILE REFERENCE: 2000-08-16
CURRENT APPLICATION NUMBER: US 69/502,330
PRIOR PILING DATE: 1999-05-07
PRIOR PLING DATE: 1999-05-07
PRIOR PLING DATE: 1999-05-07
PRIOR PLING DATE: 1999-03-23
PRIOR FILING DATE: 1999-03-23
PRIOR FILING DATE: 1999-03-13
PRIOR FILING DATE: 1999-03-13
PRIOR FILING DATE: 1999-03-13
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1304
SEQ ID NO 51
LENGTH: 448
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APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Chunakov, Ilya
APPLICANT: Chen, Annick
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
FILE REFERENCE: GENSET.051CP1
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NAME/KEX: allele

COCATION: 128

COCATION: 128

COCATION: 128

COCATION: 128

COCATION: 128

COCATION: 138

COTHER INPORMATION: 12-214-360 : polymorphic base G or C

NAME/KEX: wisc_binding

COCATION: 138:.38

COTHER INPORMATION: 12-214-360.misl, potential

NAME/KEX: wisc_binding

COTHER INPORMATION: 12-214-360.mis2, potential complement

NAME/KEX: primer_bind

COCATION: 1..20

COTHER INPORMATION: upstream amplification primer

NAME/KEX: primer_bind

COCATION: 429..48

COTHER INPORMATION: 429..48

COTHER INPORMATION: 346..370

COTHER INPORMATION: 12-214-360 potential probe

COTHER INPORMATION: 12-214-360 potential probe

COTHER INPORMATION: 12-214-360 potential probe
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Search completed: May 27, 2005, 23:57:16
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NAME/KEY: primer_bind
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NAME/KEY: primer_bind
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APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: BLALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
FILE REBERBENE: GEN-TILAKC2D1
CURRENT APPLICATION NUMBER: US/10/170,097
CURRENT FILING DATE: 2000-06-10
PRIOR PAPLICATION NUMBER: US 09/641,638
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR PILING DATE: 1999-05-07
PRIOR PILING DATE: 1999-06-07
PRIOR PELING DATE: 1999-03-03
PRIOR PILING DATE: 1999-03-03
PRIOR PILING DATE: 1999-03-03
PRIOR PILING DATE: 1999-03-03
PRIOR PELING DATE: 1999-03-03-12
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Pred. No. 1.7e-31;
0; Mismatches 1; Indels 0
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CTHER INFORMATION: upstream amplification primer
NAME/KEY: primer bind
LOCATION: 429.448
COTHER INFORMATION: downstream amplification primer, complement US-09-641-638-571
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LOCATION: 85
OTHER INFORMATION: 12-214-85 : deletion CCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc binding
LOCATION: 65..84
OTHER INFORMATION: 12-214-85.misl, potential
NAMEKEY, primer bind
                                                               PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR FILING DATE: 1999-03-23
PRIOR FILING DATE: 1999-02-12
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 1304
SEQ ID NO 571
CURRENT APPLICATION NUMBER: US/09/641,638
                 2000-08-16
3ER: US 09/502,330
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Patent No. 6794143
GENERAL INFORMATION:
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Best Local Similarity 99.4%;
Matches 155; Conservative
                      RRENT FILING DATE: 2000
IOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo Sapiens
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US-10-170-097-51
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OTHER INFORMATION: downstream amplification primer, complement
FEATURE:
NAME/KEY: misc_binding
LOCATION: 346..370

OTHER INFORMATION: 12-214-360 potential probe
US-10-170-097-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 448;
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NAME/KEY: misc_binding
LOCATION: 359..378
OTHER INFORMATION: 12-214-360.mis2, potential complement
                                                                                                                               LOCATION: 358
OTHER INFORMATION: 12-214-360 : polymorphic base G or C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 1..20
OTHER INFORMATION: upstream amplification primer
                                                                                                                                                                                                                                                LOCATION: 338..357
OTHER INFORMATION: 12-214-360.mis1, potential
LENGIN.
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
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BP377240 BM675204 CA442104 CA442104 CA442104 BP338480 BP338480	29 522.8 35.9 526 7 CR746823 CR746823 3 510.4 35.0 868 4 BI7770754 BI770754 37.0 5.0 5.0 5.0 5.0 5.0 5.0 5.0 5.0 5.0 5	507.4 34.8 570 1 A.1357378 490 33.6 490 6 CA407906 489.8 33.6 494 1 A.1159890	35 487.8 33.5 668 4 BI839159 BI839159 37.4483.8 33.2 488 5 BX282000 BX2820000 BX280000 BX	460.6 32.4 53.4 40.6 40.6 40.6 40.6 40.6 40.6 40.6 40	42 446 30.6 465 5 BM988225 BM988225 43 444.2 30.5 1124 5 BQ067351 BQ067351 44 44.2 30.4 BT012266 BT01226	439.2 30.1 906 4 BI767957	ALIGNMENTS	T 1 226	h cDNA clone CSODIO24YN10 of Placenta Cot 25-n piens (human).	ACCESSION CR620226 TRESION CR620226.1 GI:50501033 KKEYWORDS HTC: CNSLT CDNA.	Homo sapier	Buk	REFERENCE 1 (bases I to 1610) AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D. TITLE Pull-length cDNA libraries and normalization	: fliang@lifetech.			Subm BP 1	- Web : www.genoscope.cns.fr) COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime and envirohed double-strand cDNA was dipested with Not I and cloned	into the Not I and EcoR V sites of the pCWVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a	division of Invitrogen,	rce		/ / Clone = (SO) Colone Co		87.6%; Score	0	5 AGGAGATGCCAGATGATAGGGCTCCTGGGATTTCAGACCCAAGACCAGGA	Db 1 AGGAGATGGGATGTCCCAGATGATAGGGCTCCTGGGATTTCAGACCCAAGACCAGCAGGA 60
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5.1.6 Compugen Ltd.		Search time 5114 Seconds (without alignments) 10852.113 Million cell updates/sec	taataaaaatgcactcatt 1458			ters: 68479088							chance	score of the result being printed, total score distribution.		Description	CR620226 full-leng	BQ067335 AGENCOURT BQ018186 UI-H-DII- ALEAGOTE BLEAGOTE	BIS20020 603035394 BI821633 603036669	BU621880 UI-H-DF0- CA412958 UI-H-EZO-	BI838214 603083132 BI687211 III-CF-EC1	B1820/41 01 01 01 01 01 01 01 01 01 01 01 01 01	CA418829 UI-H-EZI- CA418829 UI-H-EZI- BIONEGIT 603063080	BI765751 6030651425 BI910159 603069529	BM714409 UI-E-EJO- BI912448 603291140	B1910082 603067920 B1838052 603086617 B1518752 603061934	BI910338 603068394 BP228397 BP228397	BU616457 UI-H-DF0-
GenCore vergion Copyright (c) 1993 - 2005	OM nucleic - nucleic search, using sw model	Run on: May 27, 2005, 19:21:00 ; Sear (w 10	Title: US-10-829-107-3 Perfect Bcore: 1458 Sequence: 1 gttgaggagatgggatgtcc	Scoring table: IDENTITY NUC Gapop 10.0, Gapext 1.0	Searched: 34239544 segs, 19032134700 residues	Total number of hits satisfying chosen parameters	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	ES.	2: gb_est2:* 3: gb_htc:* 4: gb_est3:*			: gb_gss2:* s the number of results	eater than or equal to the erived by analysis of the	SUMMARIES	Result Query No. Score Match Length DB ID	1277.2 87.6 1610 3	7 841.6 57.7 1134 5 759.4 52.1 816 5 736 50 5 827 1	709.6 48.7 842 4 706.2 48.4 829 4	658.4 45.2 678 5 656 45.0 674 6	9 655.8 45.0 721 4	11 654 44.9 774 4	637 43.7 663 6	616.6 42.3 816 4 604.6 41.5 852 4	604 41.4 671 4 592.6 40.6 935 4	592.2 40.6 720 4 582.4 39.9 824 4 578 39.6 721 4	22 567.4 38.9 718 4 BI310338 23 565.8 38.8 583 5 BP228397	563.8 38.7 600 5

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mamalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (Dases 1 to 1134)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM12784 row: m column: 16

High quality sequence stop: 607.
                                                                                                                  1264
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1134 bp mRNA linear EST 02-APR-2002
AGENCOURT 6767425 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5751735
S,, mRNA Bequence.
BQ067335
GCTAACATTTTTGAATTTTTTTTTTTAATTTTTAAAAGATGGTATAGTGTTCTTAAGCT 1384
                                                                                                                                                                                                                                  CACGACCTCCTCGCAAGACCGCTCTGGGAGAGAAATAAGCACTGGGAGATTGGAAGCACT
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VERSION
KEYWORDS
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AUTHORS
TITLE
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COMMENT
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                                                                                                                                                                        GTTGGCCCAAGCATGACAAGGACGTATGAAAACTTCCAGTACTTGGAGAATAAGGTGAAA
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                                                                                                                                                                                                                                                          TCCACCCCAGACTGGGCCCGGCCTCCATTTCAGCTGTGACAACCTCAGAGCCGT
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The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pTYT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (GT)18 tail. The sequence tag for this
                                                                                   816 bp mRNA linear EST 17-JUN-2002
UI-H-DT1-awk-j-06-0-UI.81 NCI_CGAP_DT1 Homo sapiens cDNA clone
BQ018186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov. The following repetitive elements were found in this cDNA sequence: 1-22, AT_rich#Low_complexity (matched compliment) Seg primer: M13 FORWARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:5890661"
/tissue_type="Metastatic Chondrosarcoma"
/dev_stage="Adult"
/lab_host="Unido [Life Technologies]"
/clone_lib="NCI_CGAP_DTI"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI_CGAP_DTI is a normalized cDNA library containing the following tissue(8): Metatastic Chondrosarcoma in Lung.
                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases I to 816) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCAGTTCATTCTG-AATGCTCCTGCGAGTCCAGCAGCTGCTGCAAGACTGAAGAAACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               library is AACTGTTCGG.
TAG TISSUE-lung metatastic chondrosarcoma
TAG_LIB=UI-H-DT1
TAG_SEQ=AACTGTTCGG"
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Llarity 99.7%; Pred. No. 6.6e-187;
Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
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Homo sapiens (human)
Homo sapiens
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Unpublished (1997)
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Best Local Similarity
Matches 771; Conserv
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                                                                                                                                                                                                                 TTGGCCCAAGCATGACAAGGACGTATGAAAACTTCCAGTACTTGGAGAATAAGGTGAAAG 305
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                                                                         GGAGATGGGATGTCCCAGATAGGGCTCCTGGGATTTCAGACCCAAGACCAGGAC
                           15;
                           Indels
  Pred. No. 2.4e-208;
0; Mismatches 49;
al Similarity 93.8%;
966; Conservative
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/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone_Tist strand cDNA was primed with a NotI-oligo(dT)
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer: Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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http://www.genoscope.cns.fr/cdna?s=CS0DI024DG05QP1&c=8440.r.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                    50.5%; Score 736; DB 1; Length 827; ilarity 91.1%; Pred. No. 8.6e-181; Conservative 0; Mismatches 0; Indels
                                                         /organism="Homo sapiens"
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT & vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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1. (Dases 1 to 827)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full.length cDNA libraries and normalization
Unpublished (2001)
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                                                                                                GAGGCTGAGAAGTACTGCCAGCTGAAGAACGCCCACCTGGTGGTCATCAACTCCAGGGAG
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                     AACTGGGTGGAGCACCAAGACAGCTGCTACTGGTTCTCTCACTCTGGGATGTCCTGGGGCC
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Contact: Genoscope
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For more information about this cluster, see
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Catarrhini; Hominidae; Homo.
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                                                                                                             CCGTGTTGCCCCAAGCATGACAGACGTTCCAGTACTTGAAAACGT
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
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603035394F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5176487 5',
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 842)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM11439 row: 1 column: 24

High quality sequence stop: 819.
                                                        760 CACTCTGGGATGTCCTGGGCCGAGGCTGAGAAGTACTGCCAGCTGAAGAACGCCCACCTG
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GAAGGGACCTGCTGCCCCGTCAACTGGGTGGAGCACCAAGACAGCTGCTACTGGTTCTCT
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                                   CACTCTGGGATGTCCTGGGCCGAGGCTGAGAAGTACTGCCAGCTGAAGAACGCCCACCTG
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
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820 GTGGTCAT 827
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/diome="UT-H-DF0-bev"-j-20-0-UI"
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The following repetitive elements were found in this cDNA sequence: 1-22, AT_rich#Low_complexity (matched compliment)

BodyA=Yes.
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                                                                                                                                                                                                                                                                                           640 AGACCTGAAGAAACTGACCTGCCAGGTGGCTACTCTCAACAATGCCTCCACTGAAGG
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
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/note="Organ: pooled brain, lung, testis; Vector:
/note="Organ: pooled brain, lung, age range 23-27;
pcMV-sPORT6; Site 1: Not1; Site 2: EcoRV (destroyed); RNA
gource anonymous pool of 6 male_brains, age fange 23-27;
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
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cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM11442 row: j column: 17
High quality sequence stop: 823.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGGTCCTTGCAGCACCAACCAACGTGGGAATCACACCCTCCAGACCTCCCACAGCTCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 CTGGTCCTTGCAGCACCAACGTGGGAATCACACCCTCCCAGACCTCCCACACCACCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGCCATCTCCTGCTGTCCCTGGGCCTCCTGCTGCTGCTGGTCATCTCTGTGTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 ATGGGATGTCCCAGATGATAGGGCTCCTGGGATTTTCAGACCCCAAGACCAGGAGTCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCAGACTGGCCCGGCCCTCCATTTCAGCTGTGACAACCTCAGAGCCGTGTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 cccadacresececesecerecerecarricascrereacaacereagesegeres
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGGTTTAAAAATGGGCCACTTCCTCCAGTCCCTCCTGCAGCGTCTCCGCTCTGGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 48.4%; Score 706.2; DB 4; Length 829; Best Local Similarity 90.5%; Pred. No. 5.3e-173; Matches 821; Conservative 0; Mismatches 3; Indels 83
                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                             1, .829
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/tissue_type="Chondrosarcoma Grade II"
/dev_stage="Adult"
/dev_stage="Chondrosarcoma Grade II"
/dev_stage="Chondrosarcoma Grade II"
/lab_host="Dh10B (Life Technologies)"
/clone_lib="NCI CGAP Ch1"
/note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI_CGAP Ch1 is a cDNA library containing the following
tissue(s): Chondrosarcoma Grade II. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
mannancector.

d(T) la tail. The sequence tag for this library is
                                                                                                             Orthospedics conthogration: Dr. M. Bento Soares, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soaresdulowa.edu The following repetitive elements were found in this CDNA sequence: 1-22, AT rich#Low_complexity (matched compliment) POLYA-Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTCTGCGAGGCTGGCCTGGGTCAGACCAGGAGAGTCACTGAGCTGCCTTTGGTGGG 1222
                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept. of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCTCACTTCCATCCAGACGCAGGTGGAATGACGACGTCTGCCAGAGGCCCTACCACTGG
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100.0%; Pred. No. 6.6e-160;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAG_TISSUE=grade-2-chondrosarcoma
TAG_LIB=UI-H-EZ0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="UI-H-EZ0-bao-b-08-0-UI"
                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAG SEQ=ATCTAATATG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 656; Conservative
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UI-H-EZO-bao-b-08-0-UI.s1 NCI CGAP_Ch1 Homo sapiens cDNA clone
UI-H-EZO-bao-b-08-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGTGACCCTGAAGGAGCCTGGAAGTGGGTGGATGGAACAGACTATGCGACCGGCTTCCA 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGTGCTCACTTCCATCCAGACGGCAGGTGGAATGACGACGTCTGCCAGAGGCCCTACCA 1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGGACCACCCGGCCACAGAAATGGCGGTGGGAGGAGCACTCTTCTCACGACCTCCTCGC 1278
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first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GTTAAGCGTC. TAG_TISSUE=subchondral bone TAG_LIS=UI-H-DATAGCGTC. TAG_LIS=UI-H-DATAGCGTC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAACTGGAAGCCAGGCCAGCCAGACGACTGGCAGGGCCACGGGCTGGGTGGAGGCGAGGA 1098
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                                                                                                                                                                                                                                                                                                          CCCCGTCAACTGGGTGGAGCACCAAGACAGCTGCTACTGGTTCTCTCACTCTGGGATGTC 858
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1 (Dases 1 to 674)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Gancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
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                                                                                                                                                                                                                                                                                                                                     CTGGGCCGAGGCTGAGAAGTACTGCCAGCTGAAGAACGCCCACCTGGTGGTCATCAACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGGGTCTGCGAGGCTGGCCTGGGTCAGACCAGCCAGGAGAGTCACTGAGCTGCCTTTGG
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                                                                                                                                                                                                                                                                                                                                                                                                        CTGGGCCGAGGCTGAGAAGTACTGCCAGCTGAAGAACGCCCACCTGGTGGTCATCAACTC
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                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                      Indels 0;
                                                                                                                                                                                                                Length 678;
                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                           Score 658.4; DB 5;
Pred. No. 1.6e-160;
0; Mismatches 1;
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CA412958.1 GI:24775609
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99.8%;
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Matches 659; Conserva
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BU687211 710 bp mRNA linear EST 07-0CT-2002 UI-CF-EC1-adv-g-09-0-UI.81 UI-CF-EC1 Homo sapiens cDNA clone UI-CF-EC1-adv-g-09-0-UI 3', mRNA sequence.
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Fax: 319 356 7171.
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                     CAGCTCCACCCCAGACTGGGCCCCGGCCCTGCCTCCATTCAGCTGTGACCACCTCAGAG
                                                                                                                                                                                               AGGACTCCAGTCACCTCTACCCCAGCTCTCCAGGACACACAGCGCTCCCAACTCTGAGTGAC
                    101 AGGACTCCAGTCACCCCTAGCCTCTCCAGGACACAGGGCTCCCAACTCTGAGTGAC
                                                                                    GTCCCACCTCTGGTCCTTGCAGCAACCAACGTGGGAATCACACCCTCCAGACCTCCCA
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/note="Organ: pooled pancreas and spleen; Vector:
pooled pancreas and spleen; Vector:
pcMv-SpoRTs; Site_1: Not1; Site_2: EcoRv (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRv site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                               TITICICITITAATITITAAAAAGAIGGIATAGIGITICITAAAGCITITITITITICCAACT 1402
                                                                                                                                                194 CCGCTCTGGGAGAGAATAAGCACTGGGAGATTGGAAGCACTGCTAACATTTTGAATTT 135
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314 GTCTGCGAGGCTGGCCTGGGTCAGACCAGGAGAGTCACTGAGCTGCCTTTGGTGG 255
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NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Lupublished (1999)

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapba-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM11559 row: o column: 07

High quality sequence stop: 719.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 721)
                                                                                                                                                                                                                                                                                               1403 TTTGAAAGTCAACTTCATGAAGGTATAATTTTTACATAAAAATGCACTCATTT 1458
                                                            254 ACCACCCGGCCACAGAAATGGCGGTGGGAGGAGGACTCTTCTCACGACCTCCTCGCAAGA
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                                                                                                                            CCGCTCTGGGAGAAATAAGCACTGGGAGATTGGAAGCACTGCTAACATTTTGAATTTT
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/lab host="DH108"
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CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems

Seq primer: M13 FORWARD

POLYAPYES.
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                                                                                     Location/Qualifiers
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TAG_SEQ=AAGTGCTTAC"
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/wol_type="mRNA"
/wol_type="mRNA"
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/clone="taxxon:9606"
/clone="tax
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Email: cgapbs-r@mail.nih.gov
Tisaue Procurement: Life Technologies, Inc.
Tisaue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MG.C. clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1437 row: k column: 12
High quality sequence stop: 769.
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Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 774)
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Best Local Similarity
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/clone lib="NIH MGC 120"
//clone lib="Organ: pooled pancreas and spleen; Vector:
//clone works site_1: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 younder.

EcoRV site is destroyed upon cloning). Average insert (EcoRV site is destroyed upon cloning). Average insert or normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library.
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44.5%; Score 649; DB 4; I
Best Local Similarity 99.4%; Pred. No. 4.5e-158;
Matches 682; Conservative 0; Mismatches 1;
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                                       organism="Homo sapiens'
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 Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Thoral to 728)
NH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Lupublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.AG.E. Consortium/LLNL at:
http://image.llnl.gov. Gclumn: 16
High quality sequence start: 7
High quality sequence stop: 728.
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                                                                                              GGGCCGAGGCTGAGAAGTACTGCCAGCTGAAGAACGCCCACCTGGTGGTCATCAACTCCA
                                                                                                                                                                     241 GTGACCTGAAGGAGCCTGGAAGTGGGTGGATGGAACAGACTATGCGACCGGCTTCCAGA
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421

284 301 344 361

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603063080F1 NIH_MGC_118 Homo sapiens cDNA linear EST 16-OCT-2001 mENA sequence.
B1905917
B1905917.1 G1:16168536
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/note="Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source leukcytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range
                                                                                                                                                                                                                                                                                                                                                                                                                  243 TGGCGGTGGGAGGACGACTCTTCTCACGACCTCCTCGCAAGACCGCTCTGGGAGAGAAAT 184
363 decaderedadreaceacercreccadadececeraceacrecerededededecere 304
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.llnl.gov
Plate: LLAMIS32 row: p column: 19
High quality sequence stop: 632.
High quality sequence stop: 632.
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1 (bases 1 to 634)

NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                 123 AAGATGGTATAGTGTTCTTAAGCTTTTTTTTTTTTTCCAACTTTTTGAAAGTCAACTTCAT
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/mol_type="mRNA"
/db_xref=taxon:9606"
/clone="IMAGE:5212290"
/tissue_type="leukocyte"
/lab_hoet="DH108"
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// Ab_xref="taxon:9606"
// Libsue="ut-H=ZL-bbg-m-10-0-UI"
// Libsue="ut-H=ZL-bbg-m-10-0-UI"
// Libsue="ut-H=ZL-bbg-m-10-0-UI"
// Libsue="ut-H=ZL-bbg-m-10-0-UI"
// Libsue="ut-H=ZL-bbg-m-10-0-UI"
// Libsue="ut-H=ZL-bbg-m-10-0-UI"
// Lib host="mbH10B" (Life Technologies)"
// Lone lib="NCI CGAP_CA2"
// NCI CGAP_CA2 is a normalized cDNA library containing the following tisue(s): Chondrosarcoma Grade II. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed that an oligo-dr prime che synthesis exertor. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the more containing and the library is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
POLYAPAYES.
                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept. of
Orthoapedics
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1 (bases 1 to 663)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
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UI-H-EZ1-bbg-m-10-0-UI.s1 NCI CGAP_Ch2 Homo sapiens cDNA clone
UI-H-EZ1-bbg-m-10-0-UI 3', mRNA sequence.
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TAG_LIB=UI-H-E21
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99.8%; Pred. No. 6.1e-155;
tive 0; Mismatches 1;
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/organism="Homo sapiens"
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1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."
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1 (bases 1 to 816)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                     69
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                                                                                                                                                                                                                                                                                                                                   CCCAGACTGGGCGCCGGCCCTCCATTTCAGCTGTGACAACCTCAGAGCCGTGTTGG
                                                                                                                                                                                                                                                                                                                                                      CCCAGACTGGGCGCCGGCCCTGCCTTTCAGCTGTGTCAACTCAGAGCCGTGTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                      241 CCCAAGCATGACAAGGACGTATGAAACTTCCAGTACTTGGAAAATAAGGTGAAAGTCCA
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                                                                                                                     1; Indels
                                                                                           4.
                                                                                       Query Match 42.6%; Score 621.4; DB 4; Best Local Similarity 99.7%; Pred. No. 7.2e-151; Matches 633; Conservative 0; Mismatches 1;
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KEYWORDS
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/organism="Homo sapiens"

/mol_type="mRNA"
/db _tref="taxon:9606"
/clone=TiMcgE:5210406"
/clone lib="NIH MGC 122"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site_1: Not!; Site_2: EcoW (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH_MGC Library."
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/Link at:
http://image.llnl.gov
Plate: LiAMI1528 row: b column: 07
High quality sequence start: 2
High quality sequence stop: 812.
Location/Qualifiers
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llarity 88.7%; Pred. No. 1.4e-149;
Conservative 0; Mismatches 4; Indels 94,
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Search completed: May 27, 2005, 23:52:45 Job time : 5121 secs

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AX409583 Sequence
M10058 Human asial
AB070933 Homo sapi
CQ725393 Sequence
BV208440 CLECSF14
BV208440 CLECSF14
BV208440 CLECSF14
BV20840 CLECSF14
U09362 Mus musculu
U09362 Mus musculu
U09362 Mus musculu
U09362 Human L-H2
AX411087 Sequence
AX5283 Human L-H2
BC17251 Homo sapi
M21770 Rat asialog
AX87915 Sequence
BD033448 Sequence
AX879588 Sequence
AX80588 Sequence
AX774853 Sequence
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JP 2002509438-A/2
26-MAR-2002
08-JUL-1999 JP 1999508710
09-JUL-1997 US 60/053080
JENNY VALLADEAU, ODILE RAVEL, ELIZABETH ESTHER MARY BATES, JOHN
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Valladeau, J., Ravel, O., Bates, E.E.M., Ford, J., Saeland, S. and Lebecque, S.J.E.
Isolated dentritic cell membrane protein genes
Patent: JP 2002509438-A 2 26-MAR-2002;
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PI SEM SABLAND, SERGE JE LEBECQUE
CC (7141/705,C12N15/12
CC Topology: Linear;
CC / note= 'short form lacks nucleotides 608-673' CC / ASGPRW (table 2) has sequence insert encoding GEE CC note= 'nucleotide 1064 of DCMP2s may be asn rather CC / note= 'nucleotide 1064 of DCMP2s may be asn rather CC / note= 'nucleotide 1064 of DCMP2s may be asn rather CC than asp at the residue numbered 270'
FH Key 257. 1204
FT CDS 257. 1204
FT misc_feature 775
FT misc_feature 775
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Isolated dentritic cell membrane protein genes.
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AC126834 Home sapi
AC107895 Home sapi
AC150057 Home sapi
AC015918 Home sapi
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BC014811 Mus muscu
AY103461 Mus muscu
AY103461 Home sapi
BC12702 CDNA encodi
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BC027858 Homo sapi
AX067341 Sequence
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ARS61599 Sequence
BC039011 Homo sapi
D50532 Homo sapien
BD135983 Isolated
                                                                                        (without alignments)
10982.078 Million cell updates/sec
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                                                                            May 27, 2005, 19:12:00 ; Search time 6433 Seconds
              GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                4708233 seqs, 24227607955 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Valladeau, J., Ravel, O., Bates, E.E.M., Ford, J., Saeland, S. and Lebecque, S.J.E.
Isolated mammalian membrane protein genes; related reagents Patent: Location/Qualifiers
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181 CAGCTCCACCCCAGACTGGGCCCGGCCTGCTTTCAGCTGTGACACCTCAGAG 240 181 CAGCTCCACCCCAGACTGGGCCCGGCCCTGCCTTTCAGCTGTGACACCTCAGAG 240 181 CAGCTCCACCCCAGACTGGGCCCGGCCCTGCCTCCATTTCAGCTGTGACAAACTCAGAG 240 241 CCGTGTTGGCCCAAGCATGACAAGGACGTATGAAACTTCCAGTACTTGGAGAATAAGGT 300 241 CCGTGTTGGCCCAAGCATGACAAGGACGTATGAAAACTTCCAGTACTTGGAGAATAAGGT 300 301 GAAAGTCCAGGGGTTTAAAAATGGGCCACTTCCTCTCCAGTACCTTCGCAGGGTTCTCCG 360	421 CTGTGTGGTTGGATTCCAAATTCCAAATTTCAGAGGACCTGGTGACCCTGAGAACAGA 480 [601 GCAGGCAGGGGTATCTGAGGAACACACTACGCAGAAGGCACACCTAGGCCACTG 660	781 CACTGAAGGAACTGCCCCGTCAACTGGGTGGAGCACCAAGACGCTGCTACTGGTT 840 781 CACTGAAGGAACCTGCTGCCCCGTCAACTGGGTGGAGCACCAAGACGCTGCTACTGGTT 840 781 CACTGAAGGAACCTGCTGCCCCGTCAACTGGGTGGAGCACCAAGACGCCCA 910 841 CTCTCACTCTCGGGATGCTCTGGGCTGAGAGTTCTTGTCTGCAAGAACGCCCA 910 842 CTCTCACTCTCGGGATGTCCTGGGCGAGGTGGAGAATTTTGTCCAAGAAGAACGCCCA 910 901 CCTGGTGGTCATCAACTCCAGGGAGGAGCAGAATTTTGTCCAGAAATATCTAGGCTCGC 960 902 CCTGGTGGTCATCAACTCCAGGGAGGAGCAGAATTTTGTCCAGAAATATCTAGGCTCCGC 960 903 ATACACCTGGATGGCCTCAGGAGGAGCAGAATTTTGTCCAGAAATATCTAGGCTCCGC 960 904 ATACACCTGGATGGCCTCAGTGACCCTGAAGGAGCCTCGAAGTGGAACTGGAACAGA 1020 1	1021 CTATGCGACCGGCTTCCAGAACTGGAAGCCAGCCAGACGACTGGCAGGGGCACGG 1080

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Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Madro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C. McDowell, J., Pearson, K., Stantripop, S., Thomas, P.J., Touchman, J.W. Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, B.D.
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                                                                                                                                                 Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov series: IRAK Plate: 82 Row: j Column: 7
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 5453683.
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/tissue type="Brain, Lung, Testis, adult, pooled
/clone_lib="NHH MGC_115"
/lab_host="DH10B"
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/product="C-type_lectin,
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/db_xref="G1:24660337"
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xref="MIM:605999"
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/db_xref="MIM:605999"
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/db_xref="taxon:9606"
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/gene="CLECSF14"
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                                             GAGAATAAGGTGAAAGTCCAGGGGTTTAAAAATGGGCCACTTCCTCCTCCAGTCCCTCG
                                                                                                         CAGCGTCTCCGCTCTGGCCCTGCCATCTCCTGCTGTCCCTGGGCCTCGGCCTGGCTGCTG
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/protein_id="macrophage lectin 2"
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WVEHQDSCYMFSHSGAWMABABLKYCQLKNAHLVVINSREGNFVQKYLGSAYTHWGLS
DPEGAMKWVDGTDYATGFQNWKFGQPDDWQGHGLGGGEDCAHFPDGRWNDDVCQRPY
                                                                          1344 bp mRNA linear PRI 10-FEB-1999 macrophage lectin 2, complete cds.
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                                                                                                                                                                                                            1 (sites)
Suzuki, V. Yamamoto, K., Toyoshima, S., Osawa, T. and Irimura, T.
Molecular cloning and expression of cDNA encoding human macrophage
C-type lectin. Its unique carbohydrate binding specificity for In
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                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (11-MAY-1995) Noriko Suzuki, The University of Tokyo,
Shculty of Pharmaceutical Sciences; 7-3-1 Hongo, Bunkyo-ku, Tokyo
113, Japan (E-mail:yamamoto@mol.f.u-tokyo.ac.jp,
Tel:03-3812-2111(ex.4872), Fax:03-3815-9344)
On Mar 10, 1997 this sequence version replaced gi:1235724.
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                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 6.1e-278;
0; Mismatches 0;
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96108853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_type="Macrophage"
/dev_stage="Adult"
208_1066
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                                                       /gene="CLECSF14"
/note="Lectin_N; Region: Hepatic lectin, N-terminal
                                                                                                                                                                                                                                                                                                                                                               1; Indels 482;
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                                                                                                                                                                       /gene="CLECSF14"
hote="CLECT; Region: C-type lectin (CTL)
carbohydrate.recognition domain (CRD)"
/db_xref="CDD:smart00034"
            LGRTLESSGSFQNDCHLCHTLRDLIGLSIQRNISKLLS"
                                                                                                                                                                                                                                                                                                               Score 857.4; DB 9;
Pred. No. 2.4e-192;
0; Mismatches 1;
                                                                                                                      /db_xref="CDD:pfam03954"
710. .844
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Best Local Similarity 73.9%;
Matches 1370; Conservative
                                                                                                        domain"
                                    misc_feature
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Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richarde, S., WcKernan, K.J., Malek, J.A., Gunaratne, P.H., Richarde, S., Vilalon, D.K., Muzny, D.M., Sodergren, E.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Miting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, M., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Schnerch, A., Schain, J.E., Schnerch, A., Schein, J.B., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

L. Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

S. Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaithersburg, Maryland;
Web Site: http://www.nisc.nih.gov/
Neb Site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Mansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Maskello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Peargeon,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Young,A., Zhang,L.-H., and Green,B.D.
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/db_xref="MIM:605999"
/translation="WIRTYENFQYLENKVKVQGFKNGPLPLQSLLQRLRSGPCHLLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGLGLLLLVI I CVVGFQNSKFQRDLVTLRTDFSNFTSNTVAEI QALTSGGSSLEETIA
SLKAEVEGFRQERQAVHSEMLLRVQQLVQDLKKLTCQVATLNNNASTEGTCCPVNWVE
HQDSCYWFSHSGMSWAEAEKYCQLKNAHLVVINSREEQVRASGTQFLRHVPFREMVLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 49 Row: m Column: 23
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 5453683.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (08-APR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: MGC help desk in the mail: capaba-remail.nih.gom.
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue type="Pancreas, Spleen, adult pooled"
/clone lib="NIH MGC 120"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="synonyms: HML2, HML, CLECSF13"
/db_xref="LocusID:10462"
251_.1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
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ACCESSION AX067341 VERSION AX067341.1 GI:12544965 KEYWORDS SOUNCE ORGANISM Homo sapiens (human) ORGANISM Homo sapiens Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 AUTHORS Yuqiu,J. and Mitcham,J.L. TITLE Compositions and methods for the therapy and diagnosis of breast cancer JOURNAL Patent: WO 0078960-A 45 28-DEC-2000; CORIXA CORPORATION (US) FEATURES 1661	Query Match 41.6%; Score 606.6; DB 6; Length 661; Best Local Similarity 98.2%; Pred. No. 7.2e-133; 0; Gaps 0; Matches 612; Conservative 1; Mismatches 10; Indels 0; Gaps 0; Qy 1 GTTGAGGAGATGGCCCCAGATGATAAGGGCTCCTGGGATTTCAGACCCAAGACCAGC 60 1 GTTGAGGAGATGGCCAGATGATGACCCAGATGATAACCAGC 60	QY 61 AGGACTCCAGTCACCTCTACCCCAGCACACAGGGCTCCCAACTCTGAGTGAC 120 Db 61 AGGACTCCAGTCACCTCTACCCCCAKTTCTCCAGGACACACACTCTGAGTGAC 120 QY 121 GTCCCACCTTGCAGCACAACCAACGAGGGAATCACACCTCCAGACCTCCCA 180 121 GTCCCACCTTGGAGCACAACCAACGAGGAATCACACCTCCAGACCTCCCA Db 121 GTCCCACCTTGGAGCACAACCAACGAGGAATCACACCTCCAGACCTCCCA	Oy 181 CAGCTCCAGACTGGGCGCGGCCCTGCCTTTCAGCTGTGACAACCTCAGAG 240	Qy 301 GAAAGTCCAGGGGTTTAAAAATGGGCCACTTCCTCCAGTCCTCCTGCAGCGTCTCCG 360 bb 301 GAAAGTCCAGGGGTTTAAAAATGGGCCACTTCCTCTCCAGTCCTTCCT	Qy 421 CTGTGTGGTTGGATTCCAAATTTCAGAGGGACCTGGTGACCCTGAGAACAGA 480 Db 421 CTGTGTGGTTGGATTCCAAATTTCAGAGGACCTGGTGACCCTGAGAACAGA 480 Qy 481 TTTAGCAACTTCACCTCAACACTGTGGAGAATCCAGGCACTGACTTCCCAGGGCAG 540	541 541	Oy 601 GCAGGCAGTATCTGAGCTCC 623
### CTCTGGGATGTCCTGGGCCGAGGCTGAGAAGTACTGCCAGCTGAAGAACGCCCACCTGGT 906	928GGAGAATTTTGTCCA 942 1060 GAGTTGGCTGGGAAGAAGTCACCACTGCCCTTCTGTCACGCAGAATTTTGTCCA 1119 943 GAAATATCTAGGCTCCGCATACACCTGGATGGGCCTCAGTGACCCTGAAGGAGCCTGGAA 1100 1120 GAAATATCTAGGCTCCCCATACACCTGGATGGGCCTCAGTGACCTGGAAGGAGCCTGGAA 1179	1003 GTGGGTGGATGGACGGACCGGCTTCCA	1039	1106 CACTTCCATCCAGACGCAGGTGGAATGACGACTCTGCCAGAGGCCCTACCACTGGGTC 1165	1226 ACCCGGCCACAGAAATGGCGGTGGGAGGAGGACTCTTCTCACGACCTCCTGGAAGACCG 1285	1600 CTCTGGGAAAATAAGCACTGGGAAAGCACTGCTAACATTTTGAATTTTTT 1659 1346 CTCTTTAAAAAAAAAAGATGGTATAGGTTCTTAAGCTTTTTATTTTTCCAACTTTT 1405 11660 CTCTTTAAATTTTAAAAAAGATGGTATAGTGTTCTTAAGCTTTTTATTTTTTTT	1406 GAAATCAACTTCATGAAGGTATAATTTTACATAATAAAATGCACTCATTT 1458

RESULT 9
RATGGSLEC
LOCUS RATGGSLEC
DEFINITION Rat Gal/GalNAc-specific lectin mRNA, complete cds.

PAT 24-JAN-2001

linear

RESULT 8
AX067341
LOCUS AX067341
DEFINITION Sequence 45 from Patent W00078960.

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Qy 627 AACACACTACCCAGAAGCACACTAGGCCACTGCCCACTGCCCACTGTGTGTG	ACCESSION ACCESS
ACCESSION JOS495 KEYMORDS GAJ/GGINAC-specific lectin. SOURCE Rattus norvegicus (Norway rat) SOURCE Rattus norvegicus (Norway rat) Bukaryota; Metzoa; Chordata; Craniata; Vertebrata; Euteleostomi; Rattus norvegicus (Norway rat) Bukaryota; Metzoa; Chordata; Craniata; Vertebrata; Euteleostomi; Rattus norvegicus (Norway rat) AUTRORS 11, M., Kurata; H., Itoh, N., Yamashina; I. and Kawasaki, T. Molecular cioning and sequence analysis of cDNA encoding the macrophage lectin specific for galactose analysis of cDNA encoding the macrophage lectin specific for galactose and N-acetylgalactosamine pubmed of them. 265 (19); 11295-11298 (1990) RUBMED 0715qinal source text; Rat (strain Wistar) adult peritoneal macrophage, cDNA to mRNN. DOTIGINAL 100-100-100-100-100-100-100-100-100-100	Query Match 30.04; Score 438; DB 10; Length 1358; Beef Local Similarity 68.14; Pred. No. 8e-93; Matches 676; Conservative 0; Mismatches 295; Indels 21; Gaps 4; Oy 210 TGCCTCCATTCAGTTCAGAGACTCAGAGCCGTGTTGGCCCAAGCATGACAAGGA 266 In

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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boquslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Bastien, V., Boquslavkiy, L., Boukhgalter, B., Brown, A., Camarate, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Dakrellano, K., Dewar, K., Dialagan, J., S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, M., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hullme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lacycque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., MacKernan, K., Major, J., Marquis, N., Marthews, C., McCarthy, M., Magoan, P., McKernan, K., Meldrim, J., Menneus, L., Mihova, T., Menga, V., Murphy, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Raback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rostetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         147006 TCGCAAGACCGCTCTGGGAGAAATAAGCACTGGGAGATTGGAAGCACTGCTAACATTT 147065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146826 AGGACTGTGCTCACTTCCATCCAGACGGCAGGTGGAATGACGACGTCTGCCAGAGGCCCT 146885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146946 TTGGTGGGACCACCCGGCCACAGAAATGGCGGTGGGAGGACTCTTCTCACGACCTCC 147005
                                                                                                                                                                                                                                               146766 TCAGGAACTGGAAGCCAGGCCAGCCAGACGACTGGCAGGGGCACGGGCTGGGTGGAGGCG 146825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGAATTTTTTTTTTTAATTTTTAAAAGATGGTATAGTGTTCTTAAGCTTTTATTTTT 1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TICCAACITITGAAAGICAACITCAIGAAGGIAIAAITITITACAIAAIAAAAAIGCACIC 1454
                                                                                                                                                                                                                                                                                                      AGGACTGTGCTCACTTCCATCCAGACGCAGGTGGAATGACGACGTCTGCCAGAGGCCCT 1154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC107895 176813 bp DNA linear HTG 27-MAR-2003
Homo sapiens chromosome 17 clone RP11-467D22 map 17, 8 ordered
                                                                                                                                                                                    1035 TCCAGAACTGGAAGCCAGGCCAGCCAGACGACTGGCAGGGGCACGGGCTGGGTGGAGGCG 1094
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                0; Gaps
                                                                Length 172095;
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AC107895.6 GI:22830372
HTG; HTGs_PHASE2; HTGS_FULLTOP; HTGS_CANCELLED.
Homo sapiens (human)
Homo sapiens
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Homo sapiens chromosome 17, clone RP11-467D22
Unpublished
                                                                DB 2;
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7
                                                                   Score 420.8; DB 2
Pred. No. 1.7e-88;
0; Mismatches 2
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                                                                   Query Match
Best Local Similarity
Matches 422; Conserv
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AC107895
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                                                                                                                                                                                                                         Direct Submitted (124-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 172095)

Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A., Cooke,P., Gradam,L., Gradam,L., Garda,S., Dodge,S., Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gord,S., Graham,L., Grand-Fleirer,N., Hagos,B., Horton,L., Hulme,W., Iliev,J., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., MacCarthy,M., Maldorla,J., Moneus,L., Mihova,T., Matthews,C., Morman,C., Norman,C., Norman,C., Norman,J., Phunkhang,P., Pierre,N., Raymond,C., Norl,D., Oliver,J., Phenson,P., Pierre,N., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Zimmer,A. and Zody,M., Waman,D., Young,G., Zainoun,J., Direct Submission Street, Cambridge, MA 02141, USA

No Septomer and Zody,M., Schauer,S., Street, Cambridge, MA 02141, USA

No Septomer and Zody,M., Street, Cambridge, MA 02141, USA

No Septomer and Zody,M., Schauer, Cambridge, MA 02141, USA

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No Septomer and Cody, Markers and Cody,M., All repeaths were identified using Repeathmaker:

Smith, AF.A., & Green, P. (196-1997)

All repeats were identified using Repeathmaker:
O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Young, G., Zainoun, J., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://ftp.genome.washington.edu/RM/RepeatMasker.html
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7630: gap of 100 bp
43794: gap of 100 bp
43894: gap of 100 bp
46168: contig of 2274 bp in length
46268: gap of 100 bp
82676: contig of 36408 bp in length
82776: gap of 100 bp
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Web site: http://www-seq.wi.mit.edu
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Biren, 30 Undates Street, Cambridge, MA 02141, USA

Biren, B. Nusbaum, C. Lander, E., Ali, A., Allen, N., Anderson, S., Barra, N., Bastien, V., Eloom, T., Boukngalter, B., Camarata, J., Chang, J., Chang, T., Boukngalter, B., Camarata, J., Chang, J., Choppel, Y., Collymore, A., Ferreira, P., FitzGerald, M., Gago, D., Galagan, J., Gard, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad, Thh, K., Liu, G., MacLean, C., Madonald, P., Major, J., Matthews, C., Matthews, C., Micol, R., North, C., Norman, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Vo, A., Wilson, B., Mu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (27-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 13, 2002 this sequence version replaced gi:22475358.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                            Submitted (24-JAN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                         Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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* This sequence will be preserved.

* This sequence will be preserved.

* To 1046: gap of 100 bp

* 1047: gap of 100 bp

* 1047: gap of 100 bp

* 105294 $50393: gap of 100 bp

* 55394 75289: contig of 24896 bp in length

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* 111998 111997: gap of 100 bp

* 11897: contig of 13497 bp in length

* 11898 111997: gap of 100 bp

* 11897: contig of 13794 bp in length

* 11898 111997: gap of 100 bp

* 11897: contig of 31967 bp in length

* 11898 111997: gap of 100 bp

* 144847 176813: contig of 31967 bp in length
Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
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Contact: sequence_submissions@genome.wi.mit.edu
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Center clone name: 467_D_22
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barra, N., Bastien, V., Bloom, T., Boguslavkiy, L., Changsalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Chopel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Plerre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kalls, C., LaRocque, K., Lamazares, R., Landers, T., Lehczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Mibnow, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, Norbu, C., Norman, C
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Homo sapiens chromosome 17, clone CTD-2545G14, complete sequence.
AC120057 GI:29611685
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Birren, B., Nusbaum, C. and Lander, E. Homo sapiens chromosome 17, clone CTD-2545G14
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                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                      DB 2; Length 176813;
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Matches 422; Conservative
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Remann, S. Sovery, P. Sencie, R. Rishe, R. Rishe, R. Rishe, C. Rogov, P. Gomann, S. Sovery, P. Spancos, R. Schamer, S. Gingbook, R. Senanni, S. Sovery, P. Spancos, R. Schamer, S. Gingbook, R. Soverni, R. Sovern
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Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission
Submitted (08-APR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 9, 2003 this sequence version replaced 91:29423939.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
center: Whitehead Institute/ MIT Center for Genome Research
Stojanovic, N., Stubbs, M.,
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/rpt_family="L2"
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5786: contig of 5786 bp in length
5886: gap of 100 bp
9996: contig of 4110 bp in length
10996: gap of 100 bp
12904: contig of 2808 bp in length
13004: gap of 100 bp
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Center clone name: 3165_0_8
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Homo sapiens chromosome 17 clone CTD-316508 map 17, 21 unordered
pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 28.9%; Score 420.8; DB 9; Length Best Local Similarity 99.5%; Pred. No. 1.7e-88; Matches 422; Conservative 0; Mismatches 2; Indels
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AC015918.10 G1:25140142
HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_CANCELLED.
HOMO sapiens (human)
Homo sapiens
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complement(11750. .11912)
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complement(11962. .12319)
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complement (11616.11749)
/rpt_family="AluJo"
                                                                                                                                                                                                                                                                                                                                          complement (12434. .12736)
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13661. .13969
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                                                                                                                                                                      /rpt_family="MIR"
complement(11305, .11615)
complement (10678. .10801)
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                                                     family="MLT1A0"
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10889. .10948
/rpt_family="MIR"
complement(10949. .
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11247. .11291
rpt family="MIR"
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ACCESSION VERSION KEYWORDS SOURCE

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Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barra, N., Beckerly, R., Boqualavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colagolo, M., Collins, S., Collymore, A., Cooke, P., Castle, A., Common, M., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Mones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McKernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M., Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA (17-NOV-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA (17-NOV-1998) Barren, B. Musbau, C., Lander, E., Alli, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Patzearalano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Faro, S., Gord, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kalla, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Mathews, C., McCarthy, M., Neldrim, J., Meneus, L., Mihova, T., Manga, W., Murphy, T., Naylor, J., Naylow, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Yous, M., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct, Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (27-mRR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Nov 20, 2002 this sequence version replaced gi:25046454.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washingcon.edu/RM/RepeatMasker.html
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Center: Whitehead Institute/ MIT Center for Genome Research
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------- Project_Information
                                                                                               1 (bases 1 to 220581)
Birren,B., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 17, clone CTD-316508
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98126 TICCAACTTTTGAAAGTCAACTTCATGAAGGTATAATTTTTACATAATAAAAAATGCACTC 98067
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/note="Wethod: conceptual translation with partial peptide
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FLQNRLANVYSWIGITTDQNGPWRWVDGTDFEKGFKNWAPLQPDNWFGHGLGGGEDCAH
ITTGGPWNDDVCQRTFRWICEMKLAKES"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 104199] from the original journal article. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18; Gaps
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/gene="galactose and N-acetylgalactosamine-specific
lectin, MwGL"
171. .1085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'gene="galactose and N-acetylgalactosamine-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sato, M., Kawakami, K., Osawa, T. and Toyoshima, S. Molecular cloning and expression of cDNA encoding a galactose/N-acetylgalactosamine-specific lectin on mouse
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J. Biochem. 111 (3), 331-336 (1992)
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/db_xref="taxon:10095"
1. .1414
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macrophage, mRNA, 1414 ntl.
S36676
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                                                                                                                               98066 ATTT 98063
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Best Local Similarity
Matches 635; Conserv
                                                                                              1455 ATTT 1458
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ORGANISM
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                                 contig of 4124 bp in length
gap of 100 bp
contig of 5130 bp in length
contig of 100 bp
contig of 106 bp
gap of 100 bp
contig of 15785 bp in length
gap of 100 bp
gap of 100 bp
gap of 100 bp
gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                           contig of 665 bp in length

gap of 100 bp

contig of 22647 bp in length

gap of 100 bp

contig of 4477 bp in length

gap of 100 bp

contig of 1158 bp in length

gap of 100 bp

contig of 1175 bp in length

contig of 11775 bp in length

gap of 100 bp

contig of 11775 bp in length

gap of 100 bp

contig of 303 bp in length

gap of 100 bp

contig of 3061 bp in length

gap of 100 bp

contig of 3061 bp in length

gap of 100 bp
                                                                                                                                                                                                                                                                                gap of 100 bp

: contig of 33357 bp in length

: gap of 100 bp

: contig of 13184 bp in length

: gap of 100 bp

: contig of 6655 bp in length

: gap of 100 bp
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                                                                                                                                                                                            Contiguate 100 bp gap of 100 bp contiguate of 7219 bp in length gap of 100 bp contiguate of 7078 bp in length
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                     100 bp
of 4124 bp in length
100 bp
   8886 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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/db_xref="taxon:9606"
/chromosome="17"
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gap of 100
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Brownstein, M.J.,
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                962 TACACCTGGATGGGCCTCAGTGACCCTGAAGGAGCCTGGAAGTGGGATGGAACAGAC 1021
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klauener, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                          TGTGTGGTTGGATTCCAAATTTCAGAGGGACCTGGTGACCTGAGAACAGAT
                                                       324 TCCGTGATTGGATCCCAAAATTCCCAGTTAAGGAGGAGCTAGGCACCTGAGAGGCACT
                                                                                                                                  TITIAGCAACTICACCTCAAACACTGTGGCGGAGATCCAGGCACTGACTICCCAGGGCAGC
                                                                                                                                                                                                                                                                                                                                                                CAGGCAGGGGTATCTGAGCTCCAGGAACACACTACGCAGAAGGCACACCTAGGCCACTGT
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SOURCE
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 31 Row: g Column: 11
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6754687.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="Locusid:17312"
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ANLKNNGSEVACCPLHWTEHBGSCYWFSESSEKSWPEADKYCRLENSHLVVVNSLEEQN
                            Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Vallalon, D.K., Miting, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Wadan, A., Young, A.C., Shevchenko, Y. Bouffard, G.G., Blakealey, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Samilus, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A. Generation and initial analysis of more than 15,000 full-length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (01-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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/clone="WGC:25983 INAGE:4456238"
/fissue_type="Mammary tunnor. Metallothionien-TGF alpha
model. 10 month old virgin mouse. Taken by biopsy."
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Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Prepared by: The Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
    Toshiyuki, S.
Usdin, T.B.,
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/protein id="AAH14811.1"
/db_xref="GI:15928688"
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/mol_type="mRNA"
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1557: 1069
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FLQNRLANVVSWIGLTDQNGPWRWVDGTDPEKGFKNWAPLQPDNWFGHGLGGGEDCAH ITTGGPWNDDVCQRTFRWICEMKLAKES"

ORIGIN

Search completed: May 27, 2005, 22:27:25 Job time : 6442 secs

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Adf17999 Lung canc
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ALIGNMENTS

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	₹	chromosomal abnormality; expression misregulation;	
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	ž Ľ	Dendritic cell membrane proteins - used to treat conditions asso	ciate
	L A	with abnormal physiology or development.	
	PS PS	Disclosure; Page 68-69; 82pp; English.	
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	ខ្ល	Dendritic cell membrane protein 1 (DCMP1) and DCMP2 nucleic acid	B car
	ပ္ပ	used as markers for distinguishing cell types, including genomic	aBbe

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be used to detect chromosomal abnormalities. The proteins can be used to diagnose disorders associated with expression misregulation. They can also be used to treat conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions or degeneration and atrophy may be modulated using the proteins, proteins may also play a role in regulation or development of haematopoietic cells
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                                                                                                                                                                      Sequence 1458 BP; 349 A; 406 C; 388 G; 315 T; 0 U; 0 Other;
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Best Local Similarity 100.
Matches 1458; Conservative
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The invention relates to human novel polynuclectides and associated polypeptides. The polynuclectides and polypeptides are useful for treating inflammatory conditions such as arthritis, mephritis, Crohn's disease, ischaemia-repertusion injury, shock, sepsis, immune responses and cancer and for promoting wound healing. The sequences are used to induce the proliferation of neural cells and regeneration of nerve and brain tissue, and are useful for the treatment of central and peripheral nervous system disease, Huntington's disease and amyotrophic lateral scleasis. The sequences are involved in chemotactic or chemokinetic activity, regulation of haematopolesis, treatment of myeloid or lymphoid cell disorders and platelet disorders such as thrombocytopenia, regeneration of home, cartilage, tendon, ligament and/or nerve tissue repair, healing of burns, incisions, ulcers, treatment of steoporosis, osteoparthitis, bone degenerative disorders and periodontal disease. The sequences of the invention are also useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, immune deficiencies and disorders infections, autoimmune disorders e.g. multiple sclerosis and myasthenia including severe combined immunodeficiency (SCID), bacterial or fungal infections autoimmune disorders e.g. multiple sclerosis and myasthenia and coagulation disorders. Sequences ABK944892 represent human novel polynucleotides of the invention Novel nucleic acids and polypeptides for diagnosis, treatment of inflammatory, autoimmune, nervous system, myeloid or lymphoid cell disorders, cancer and promoting wound healing. Wang J, Asundi V, Liu C, Zhou P, Drmanac RT; Claim 1; Page 420-422; 672pp; English Goodrich RW, WPI; 2002-508509/54. P-PSDB; ABG66703. (HYSE-) HYSEQ INC > Tang YT, Yamazaki

Seguence 1531 BP; 370 A; 419 C; 401 G; 341 T; 0 U; 0 Other;

420 114 AGGACTCCAGTCACCTCTACCCCAGCTCTCCAGGACACAGCGCTCCCAACTCTGAGTGAC 120 AGGACTCCAGTCACCTCTACCCCAGCTCTCCAGGACACAGGCGCTCCCAACTCTGAGTGAC 174 234 CAGCTCCACCCCAGACTGGGCGCCGGGCCCTGCCTTTCAGCTGTGACAACCTCAGAG 240 294 CCGTGTTGGCCCAAGCATGACAAGGACGTATGAAAACTTCCAGTACTTGGAGAATAAGGT 300 GAAAGTCCAGGGGTTTAAAAATGGGCCACTTCCTCTCCAGTCCCTCCTGCAGCGTCTCCG 360 crcreecccreccarcrecrerereceresecreecerecreerecreerear 474 CTGTGTGGTTGGATTCCAAAATTCCAAATTTCAGAGGGACCTGGTGACCTGAGAACAGA 480 GICCCACCTCTGGTCCTTGCAGCACAACCAACGTGGGAATCACACCCTCCAGACCTCCCA 180 354 GAAAGTCCAGGGGTTTAAAAATGGGCCACTTCCTCTCCAGTCCCTCCTGCAGCGTCTCTG 414 GTTGAGGAGATGTGGATGTCCCAGATGATAGGGCTCCTGGGATTTCAGACCCAAGACCAGC GTCCCACTCTGGTCCTTGCAGCACAACCAACGTGGGAATCACACCTCCAGACCTCCCA CAGCTCCACCCCAGACTGGGCGCCGGCCTGCCTCCATTTCAGCTGTGACAACCTCAGAG CCGTGTTGGCCCAAGCATGACAAGGACGTATGAAAAACTTCCAGTACTTGGAGAATAAGGT CTCTGGGCCCTGCCATCTCCTGCTGTCCCTGGGCCTCGGCCTGCTGCTGCTGGTCATCAT GTTGAGGAGATGGGATGTCCCAGATGATAGGGCCTCCTGGGATTTCAGACCCAAGACCAGC Gaps 9 Length 1531; 3; Indels DB 6; Score 1434.2; Pred. No. 0; 0; Mismatches Query Match 98.4%; Best Local Similarity 99.2%; Matches 1455; Conservative 421 55 61 115 121 175 181 235 241 295 301 355 361 415 a 8 S 8 ઠ 셤 ò ઠે 요 ò 원 ò 8 8 ò

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dendritic cell membrane protein 1 (DCMD1) and DCMD2 nucleic acids can be used as markers for distinguishing cell types, including genomic aspects of cells, as well as mENA and protein expression patterns. They can also be used to detect chromosomal abnormalities. The proteins can be used to detect chromosomal abnormalities. The proteins can be used to disorders associated with expression misregulation. They can also be used to treat conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions or degeneration and atrophy may be modulated using the proteins. The proteins may also play a role in regulation or development of haematopoietic cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     164 CCAACGTGGGAATCACACCTCCAGACCTCCCACAGCTCCACACCTGGGCGCCGGC 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCTGCCTCCATTTCAGCTGTGACAACCTCAGAGCCGTGTTGGCCCAAGCATGACAAGGAC 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87
                                                                                                                                                                                            ss; primate; dendritic cell membrane protein; DCMP1; DCMP2;
chromosomal abnormality; expression misregulation;
abnormal proliferation; regeneration; degeneration; haematopoietic cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dendritic cell membrane proteins - used to treat conditions associated with abnormal physiology or development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 TAGGGCTCCTGGGATTTCAGACCCAAGACCAGCAGGACTCCAGTCACCTCTACCCCAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCAACGTGGGAATCACACCCTCCAGACCTCCCACAGCTCCACAGACTGGGCGCCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 147;
                                                                                                                                                    Variant primate DCMP2 C-lectin family gene nucleotide sequence.
                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
273. 1094
/*tag= a
/product= "DCMP2 C-lectin family gene protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence 1370 BP; 355 A; 360 C; 353 G; 302 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1108; DB 2; ]
Pred. No. 1.2e-276; 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ford J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 76-78; 82pp; English.
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                      BP
                        CDNA; 1370
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Best Local Similarity 89.4%;
Matches 1288; Conservative
                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SCHE ) SCHERING CORP
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                      AAX04868 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAW88129.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9902562-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-JUL-1997;
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The invention relates to human NOVX polypeptides and the polynucleotides encoding them. The polypeptides, polynucleotides and antibodies that bind immunospecifically to the polypeptides are useful in the manufacture of a medicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder. The sequences are useful for treating, preventing or diagnosing diseases such as metabolic disorders, tababetes, obsentity, infectious diseases, external, fungal, helmithic, and protozoal), anorexia, cancer, cardiovascular disorders (e.g. hypertension, atherosclerosis), neurodegenerative disorders (e.g. hypertension, atherosclerosis), neurodegenerative disorders, osteoarthritis, haematopoietic disorders, inflammatory skin disorders, asthma and various dyslipidemias. The nucleic acids and polypeptides may also be used as targets for the identification of small molecules that modulate or inhibit es, neuropsensis, cell differentiation, cell proliferation, haematopoiesis, wound healing and angiogenesis, and in the generation of antibodies that bind immunospecifically to NOVX substances for use in therapeutic or diagnostic methods. The nucleic acids are further used as hybridisation probes, and in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. Sequences ACA10111-ACA10156 represent human NOVX polynucleotides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGGTGGCTACTCTCAACAACAAT-----GCCTCCACTGAAGGGACCTGCTGCCCCG 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTCTCCAGTCCCTCCTGCAGCGTCTCTGCTCTGGGCCCTGCCATCTCCTGCTGTCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAACTICCAGTACTIGGAGAATAAGGIGAAAGICCAGGGGTITAAAAAIGGGGCACTIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated NOVX polypeptides and polynucleotides, useful for preventing, disagnosing or treating NOVX-associated disorders, e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease, asthma, or infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCCATTTCAGCTGTGACAACCTCAGAGCCGTGTTGGCCCCAAGCATGACAAGGACGTATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1039.2; DB 8; Length 1072;
Pred. No. 7.5e-259;
0; Mismatches 3; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1072 BP; 247 A; 297 C; 313 G; 215 T; 0 U; 0 Other;
                                                                                                                                                                Claim 20; Page 169-170; 340pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 71.3
Best Local Similarity 98.9
Matches 1060; Conservative
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                      TITITITICICITITAAITITIAAAAAGAIGGIAIAGIGITICITAAGCITITITITITICC 1285
                                                                                                                   AACTTTTGAAAGTCAACTTCATGAAGGTATAATTTTTTACATAATAAAAAAATGCACTCATTT 1345
                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; NOVX; gene; ss; metabolic disorder; diabetes; infectious disease; obesity; anorexis; cancer; cardiovascular disorder; asthma; neurogenesis; neurodegenerative disorder; epilepsy; immune disorder; osteoarthritis; haematopoietic disorder; inflammatory skin disorder; dyslipidemia; haematopoietis; wound healing; angiogenesis; bacterial infection; viral infection; fungal infection; helminthic infection; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SG;
                                                                                           AACTTTTGAAAGTCAACTTCATGAAGGTATAATTTTTTACATAATAAAATGCACTCATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protozoal infection; hypertension
                                                                                                                                                                                                                                                           ВР
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04-MAY-2001; 2001US-0288900P.
07-MAY-2001; 2001US-028908PP.
15-MAY-2001; 2001US-029189P.
16-MAY-2001; 2001US-029189P.
16-MAY-2001; 2001US-029189P.
21-MAY-2001; 2001US-0292301P.
22-MAY-2001; 2001US-0292301P.
23-MAY-2001; 2001US-02928PP.
23-MAY-2001; 2001US-029434P.
31-MAY-2001; 2001US-029434P.
31-MAY-2001; 2001US-02948BP.
31-MAY-2001; 2001US-02989BP.
31-MAY-2001; 2001US-02989BP.
31-MAY-2001; 2001US-02989BP.
31-MAY-2001; 2001US-02989BP.
31-MAG-2001; 2001US-031338BP.
21-AUG-2001; 2001US-031338P.
21-AUG-2001; 2001US-031338P.
21-AUG-2001; 2001US-031348P.
27-SEP-2001; 2001US-032586SP.
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01-MAY-2002;
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Gaps 6; 272

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Polymucleotide sequences AAF17982 - AAF18424 encode human lung cancer associated proteins represented in AAB58106 - AAB58548. Lung cancer associated proteins and polymucleotide sequences, their agonists, and antiquoists may have neuroprotective; cytostatic; cardioactive; and antiquoists may have neuroprotective; cytostatic; cardioactive; and energy; gastrointestinal general; nephrotropic; antiinfective; gynecological; or antibacterial activity. The invention also includes antibodies specific for the protein or polymucleotide sequences. The lung cancer associated polymucleotide sequences may be used for detection of lung cancer, chromosome contactification, as chromosome markers, and for numerous other diagnostic or research purposes. The proteins may be used to treat diagnostic or research purposes. The proteins may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders. The proteins may also be used in the treatment of wounds and infectious diseases.

Polymucleotide sequences AAF18425 - AAF18433 and poptide AAB58549 are used in the course of the invention for the identification and
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llarity 89.8%; Pred. No. 3.6e-177;
Conservative 6; Mismatches 6;
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CCGAGGCTGAGAAGTACTGCCAGCTGAAGAACGCCCACCTGGTGGTCATCAACACTCCAGGG
                                                                                                                                                                                                 AGGAGCAGAATTTTGTCCAGAAATATCTAGGCTCCGCATACACCTGGATGGGCCTCAGTG
                                                                 AGGAGCAGAATTTTGTCCAGAAATATCTAGGCTCCGCATACACCTGGATGGGCCTCAGTG
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New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, diabetes, atherosclerosis, asthma or AIDS, and in chromosome mapping, tissue typing or pharmacogenomics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to human NOVX polypeptides and the polynucleotides encoding them. The polypeptides, polynucleotides and antibodies that bind immunospecifically to the polypeptides are useful in diagnosing, treating or preventing NOVX-associated disorders such as cardiomyopathy, atherosclerosis, hypertension, scleroderma, obesity, cancer, diabetes, multiple sclerosis, infections, anorexia, cancer-associated cachexia, neurodegenerative disorders (e.g. Alzheimer's disease or Parkinson's disease), haematopoietic disorders and wasting disorders. The polynucleotides are also used as hybridisation probes, in chromosome mapping and in tissue typing. The polypeptides are also useful as vaccines. This sequence represents a human NOVX polynucleotide of the
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49.2%; Score 717.6; DB 12;
Best Local Similarity 87.2%; Pred. No. 1.8e-175;
Matches 933; Conservative 0; Mismatches 4;
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MALYANKAR U M.
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RIEGER D K.
SHENOY S G.
SHIKKETS R A.
SPYTEK K A.
TAUPIER R J.
BURGESS C E.
CASMAN S J.
CHAPOVAL A.
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GUNTHER E.
GUO X S.
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LEPLEY D M.
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  -------CAGTICATICIGAAAIGCICCIGCGAGICCAGCA 669
                                                               GCTGGTGCAAGACCTGAAAAACTGACCTGCCAGGTGGCTACTCTCAACAACAACAAGCCT
                                                                                                                                                    ccacrgaagggaccrgcrgccaygrcaacrggaggaggaggagaggrgcraggr
                                                                                                                                                                                           TCTCTCACTCTGGGATGTCCTGGGCCGAGGCTGAGAAGTACTGCCAGCTGAAGAACGCCC
                                                                                                                CCACTGAAGGGACCTGCTGCCCCGTCAACTGGGTGGAGCACCAAGACAGCTGCTACTGGT
                                      GCTGGTGCAAGACTGAACTGACTGCCAGGTGGCTACTCTCAACAACAAT-GCCT
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ANDERSON D W.
BOLDOG F L.
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Human; NOVX; gene; ss; metabolic disorder; diabetes; infectious disease; bobesity; anorexis, cancer; cardiovascular disorder; asthma; neurogenesis; neurodegenerative disorder; capilepsy; immune disorder; osteoarthritis; haematopoietic disorder; inflammatory skin disorder; dyslipidemia; haematopoiesis; wound healing; anglogenesis; bacterial infection; viral infection; hupertension; helminthic infection; atherosclerosis; protozoal infection; hypertension.

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CCTGAAGGAGCCTGGAAGTGGGTGGATGGAACAGACTATGCGACCGGCTTCCAGAACTGG 1045
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                                         393 GCCTCGGCCTGCTGCTGCTGTCATCTGTGTGGTTGGATTCCAAAATTCCAAATTTC
                                                                                               453 AGAGGGACCTGGTGACCCTGAGAACAGATTTTAGCAACTTCACCTCAAACACTGTGGCGG
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2001US-0292587P. 2001US-0293107P. 2001US-0294434P. 2001US-0294834P. 2001US-0298988P.

22-MAY-2001; 23-MAY-2001; 29-MAY-2001; 30-MAY-2001; 31-MAY-2001; 18-JUN-2001; 31-JUL-2001;

2001US-0289087P. 2001US-0290753P.

2001US-0291189P 2001US-0291243P

2001US-0288900P

WO200290504-A2

02-MAY-2002;

14-NOV-2002

sapiens

Homo

2001US-0292001P. 2001US-0292374P.

15-MAY-2001; 16-MAY-2001; 18-MAY-2001; 21-MAY-2001; 31-JUL-2001; 2001US-031838P.
21-AUG-2001; 2001US-031338P.
21-AUG-2001; 2001US-031338P.
21-AUG-2001; 2001US-031338P.
21-AUG-2001; 2001US-031397P.
21-AUG-2001; 2001US-0312201P.
25-SEP-2001; 2001US-0323314P.
27-SEP-2001; 2001US-032368P.
27-SEP-2001; 2001US-032368P.
21-NOV-2001; 2001US-033682P.
21-NOV-2001; 2001US-033682P.
21-NOV-2001; 2001US-033682P.
21-NOV-2001; 2001US-033682P.
21-NOV-2001; 2001US-033688P.
21-NOV-2001; 2001US-033688P.
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21-NOV-2001; 2001US-033688P.
21-NOV-2001; 2001US-033688P.
21-NOV-2001; 2001US-03468P.
21-NOV-2001; 2001US-0346P.
21-NOV-2001; 2001US-03234P.
21-NOV-2001; 2001US-0

Millet I, Padigaru M, Patturajan M, Pena CEA, Rieger DK, Shenoy SG; Shinkete RA, Spytek KA, Taupier RJ, Vernet CAM, Voss EZ; Schusen BD; Schusen BD; Vernet CAM, Voss EZ; Serhusen BD; Voss EZ; Voss EZ;

Claim 20; Page 169; 340pp; English.

asthma, or infections

The invention relates to human NOVX polypeptides and the polynucleotides encoding them. The polypeptides, polynucleotides and antibodies that bind immunospecifically to the polypeptides are useful in the manufacture of a medicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder. The sequences are useful for treating, preventing or diagnosing diseases such as metabolic disorders, diabetes, obesity, infectious diseases (viral, bacterial, fungal, helminthic, and protozoal), anorexia, cancer, cardiovascular disorders (e.g. hypertension, atherosclerosis), neurodegenerative disorders (e.g.

Human NOVX polynucleotide #44.

(first entry)

02-JUN-2003

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standard; cDNA; 820

ACA10154 ACA10154;

RESULT 7 ACA10154

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GGGTCTGCGAGGCTGGCCTGGGTCAGACCAGGAGAGTCACTGAGCTGAGCTGCCTTTGGTG 1220
                                  760 GGGTCTGCGAGGCTGGGTTGGGTCAGACCAGCGAGAGTCACTGAGGTACCTTTGGTG 819
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2001US-029201P
2001US-0292314P
2001US-0293107P
2001US-029410P
2001US-0294434P
2001US-0294434P
2001US-0394827P
2001US-0313388P
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2001US-0288900P.
2001US-0289087P.
2001US-0290753P.
2001US-0291189P.
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2001US-0332129P.
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BOLDOG F L.
BURGESS C E.
CASMAN S J.
CHAPOVAL A.
EDINGER S R.
GERLACH V.
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GUNTHER E.
GUO X S.
KEKUDA R.
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04-MAY-2001;
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14-DEC-2001;
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Alzheimer's disease, Parkinson's disease), epilepsy, immune disorders, osteoarthritis, haematopoietic disorders, inflammatory skin disorders, asthma and various dyslipidemias. The nucleic acids and polypeptides may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, cell differentiation, cell proliferation, haematopoiesis, wound healing and angiogenesis, and in the generation of antibodise that bind immunospecifically to NoVX substances for use in therapeutic or diagnostic methods. The nucleic acids are further used as hybridisation probes, and in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. Sequences ACA10111-ACA10156 represent human NOVX polynucleotides of the invention
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                                                                                                                                                                                               Score 714.6; DB 8; Length 820;
Pred. No. 1e-174;
0; Mismatches 9; Indels 81
                                                                                                                                                                     Seguence 820 BP; 181 A; 227 C; 243 G; 169 T; 0 U; 0 Other;
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ther E, Guo XS;
Miller CE;
eger DK, Shenoy SG;
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                                                                                                                                                                                                                                                                                 FL, Burgess CE, Casman S Gorman L, Gunther E, G Malyankar UM, Miller CE 1, Pena CEA, Rieger DK, Vernet CAM, Voss EZ;
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                                                                                                                                                                                                                                                                                Alsobrook JP, Anderson DW, Boldog FL,
Chapoval A, Edinger SR, Gerlach V, Go
Kekuda R, Lepley DM, Li L, Liu X, Mai
Millet I, Padigaru M, Patturajan M, Pa
Shimkets RA, Spytek KA, Taupier RJ, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20; SEQ ID NO 87; 219pp; English
                                             MALYANKAR U M.
MILLER C E.
MILLET I.
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PADIGARU M.
PADIGARU M.
PENA C E A.
RIEGER D K.
SHENOY S G.
SHIMKETS R A.
SPYTEK K A.
TAUPIER R J.
VERNET C A M.
VOSS E Z.
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   LEPLEY D M.
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The invention relates to a novel method of predicting at least one toxic effect of a compound. The method comprises a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database compound, and comparing the gene information given in the specification. The methods are useful for predicting at least one toxic effect of a compound, predicting the progression of a toxic effect of a compound, predicting the renal coxicity of a compound, or identifying toxicity markers in tissues or cells exposed to known renal toxin. The genes are useful as toxicity markers in drug screening and toxicity assays, in monitoring disease or physiological states, or disease progression. This polynucleotide represents a rat DNA sequence relating to the toxic effect database described in the specification. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the World Intellectual Property
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210 TGCCTCCATTTCAGCTGTGACAACCTCAGAGCC---GTGTTGGCCCAAGCATGACAAGGA 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Predicting at least one toxic effect of a compound, useful for toxicity modeling, comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database.
Toxic effect; gene expression profile; renal toxicity; toxicity marker; database; drug screening; toxicity assay; rat; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.0%; Score 43%; DB 10; Length 135%; 68.1%; Pred. No. 7.4e-103; ive 0; Mismatches 295; Indels 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1358 BP; 340 A; 325 C; 365 G; 328 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Castle A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Higgs B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Johnson K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; Page; 446pp; English.
                                                                                                                                                                                                                                                                                                                                                                   2001US-0336144P
2001US-0340873P
2002US-0357842P
2002US-0357844P
2002US-0357844P
2002US-0377844P
2002US-0370244P
2002US-0370206P
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2001US-0303810P.
2001US-0315047P.
2001US-0330462P.
2001US-0330462P.
2001US-0330867P.
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Matches 676; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Porter M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENE-) GENE LOGIC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-148464/14.
                                                    Rattus norvegicus.
                                                                                   WO200295000-A2
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28-AUG-2001;
27-SEP-2001;
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                                                                                                                                                                                                                                                                                                                       22-OCT-2001;
01-NOV-2001;
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                                                                                                                                                                                                                                                                                                                                                                        06-DEC-2001;
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15-MAR-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mendrick D,
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                                                                                                                    28-NOV-2002
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                                                                                                                                  The present invention provides the coding sequences for a number of breast cancer related proteins. These can be used in vaccinations against, diagnosis of and treatment of cancer, particularly breast cancer
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                                                                                                                                                                                                                                  Query Match 41.6%; Score 606.6; DB 4; Length 661; Best Local Similarity 98.2%; Pred. No. 9.6e-147; Matches 612; Conservative 1; Mismatches 10; Indels 0
                                                                                                                                                                                                    Sequence 661 BP; 156 A; 199 C; 166 G; 139 T; 0 U; 1 Other;
                                                New polynucleotides encoding breast tumor specific p
prevention, treatment and diagnosis of breast cancer
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                                                                                                     Claim 25; Page 133-134; 165pp; English
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                 WPI; 2001-041426/05
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Elashoff

ss; gene; gene therapy; human diagnostic and therapeutic polynucleotide; dithp.

12-SEP-2003; 2003WO-US028227

WO2004023973-A2

Homo sapiens.

2002US-0410259P.

12-SEP-2002; 12-SEP-2002;

(INCY-) INCYTE CORP.

Human diagnostic and therapeutic polynucleotide SEQ ID NO:101

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1107 ACTICCAICCAGACGCAGGTGGAATGACGACGICTGCCAGAGGCCCTACCACTGGGTCT 1166
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Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F; Hartbahorne TA, Suchorolski MT, Alues CM, Pittes SJ, Bidee LV; Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP; Stevens KA, Blanchard JL, Panezer SR, Wang X, Au AP, Gerstin EH; Peralte CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL; Lagace RB, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES; Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen

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The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine to incommune/inflammatory disorder, developmental disorders, or autoimmune/inflammatory disorder, developmental disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp conflections caused by virus, bacteria, fungi or parasite. The dithp confless may also be used in genetic amapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline colymorphisms, as molecular weight markers, and for somatic or germline sequence deta for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPPO at www.wipo.int/pct/en/sequences/listing.htm
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The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human control invention may have a use in gene therapy. The human chiagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnost a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine catorimne/inflammatory disorder, developmental disorder, endocrine disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp cological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represents a dithp polymucleotide of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
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therapy; human diagnostic and therapeutic polynucleotide;

sa; gene; gene

WO2004023973-A2

Homo sapiens

Human diagnostic and therapeutic polynucleotide SEQ ID NO:99.

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641 AAGATCACTCCAGCCTGCTCCACGTGAAGCAGTTCGTGTCTGACCTGCGGAGCCTGA
                                                                             666 ACTGCCCATCTGTGTGTCCCAGTTCATTCTGAAATGCTCCTGCGAGTCCAGCAGCTGG
                                                                                                    GCTGTCAGATGGCGCCCTCCAGGCCAATGGTAAGGAGGCCAGCCCGGCCCGCTCTCTGC
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progression of liver cancer, hepatocellular carcinoms or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from tumour in a patient, and differentiating metastatic liver cancer from expression of two or more genes represented in ABN93503-ABN97455 in a tissue sample. The method of the invention has hepatocropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug efficacy and drug metabolism. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at
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                                   carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in a liver tissue sample.
                    liver cancer, hepatocellular
                                                                                                                                      The invention relates to a novel method for diagnosing and detecting the
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Pred. No. 2.4e-88;
0; Mismatches 245; Indels
                  detecting the progression of
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ftp.wipo.int/pub/published_pct_sequences
                                                                                               Claim 1; SEQ ID NO 2230; 298pp; English.
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and genomic fragments and in research and diagnostic applications. The array can detect changes in expression in a large number of genes coding for different signaling pathway populations which can be used to diagnose various diseases including cancer e.g. adenocarcinoma and leukaemia, immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease and Parkinson's disease. The present sequence represents a polymucleotide probe of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at
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                                                                                                                                                                                                                                     Score 382; DB 10; Length 1277;
Pred. No. 2.4e-88;
0; Mismatches 245; Indels 87,
                                                                                                                                                                                                      U; 0 Other;
                                                                                                                                                                  segdata.uspto.gov/seguence.html?DocID=06500938B1
                                                                                                                                                                                                     Sequence 1277 BP; 271 A; 394 C; 378 G; 234 T; 0
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signalling pathway population; cancer; adenocarcinoma; leukaemia;
immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
                                                                                                                                                                      GECCECTEGAACGACGACGTCTGCCAGAGGCCCTACCGCTGGGTCTGCGAGAGACAGAGCTG
 TGCCAGCTGAAGAACGCCCACCTGGTGGTCATCAACTCCAGGGAGGAGGAGAATTTTGTC
                                                                                                          cadeaceacaradecererenadeacerenadaresecrecaceaceanadesecerese
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                                     716 TGCCGGCTGGAGGACGCGCACCTGGTGGTCACGTCCTGGGAGGAGCAGAAATTTGTC
                                                                       CAGAAATATCTAGGCTCCGCATACACCTGGATGGGCCTCAGTGACCCTGAAGGAGCCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           signalling pathway polynucleotide probe SEQ ID NO 1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 1186; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                  GGTCAGACCAGCCAGGAG 1198
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The invention relates to a composition of polymucleotide probes comprising first polymucleotide probes comprising at least a portion of a gene encoding a receptor-like polymetide, second polymucleotide probes comprising at least a portion of a gene encoding a transducing polymetide and third polymucleotide probes comprising at least a portion of a gene encoding an effector-like polypeptide. The probes of the composition are useful as array elements in a microarray for monitoring the expression of target polymucleotides. The microarray is useful in the diagnosis and treatment of cancer, an immunopathology or a neuropathology. It can also be used for drug discovery and development, toxicological and carcinogenicity studies, forensics or pharmacogenomics. Microarrays can also be used for monitoring the progression of diseases that may be associated with the altered expression of signathing pathway polypeptides. The composition can also be used to purify a subpopulation of mRNNA, cDNAA, or genomic fragments in a sample. The expression profile is also useful for the diagnosis and treatment of cancer, e.g. cancers of the adrenal gland, bladder, bone, bancement, when it, breast or cervix, an immunopathology, e.g. AIDS, diabetes, pancreatitis, osteoporosis or ulcerative colitis, or a neuropathology, e.g. dementia, amnesia,
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nntion. Note: The sequence data for rinted specification but was from USPTO at
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                                                                                                              Length 1277;
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                                                                                                              Score 382; DB 12; ]
Pred. No. 2.4e-88;
0; Mismatches 245;
      epilepsy, Alzheimer's disease or depression. human polymucleotide probe of the invention. this patent did not form part of the printed obtained in electronic format directly from U
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Sequence 9, Applisequence 7, Applisequence 17, Applisequence 15, Applisequence 169, Applisequence 169, Applisequence 169, Applisequence 1642, Applisequence 1642, Applisequence 46, Applisequence 46, Applisequence 49, Applisequence 51, Applisequence 50, Applisequence 11324, Apslight 56, Applisequence 11324, Applisequence 11324, Applisequence 11324, Applisequence 11324, Applisequence 11324, Applisequence 1685, Applisequence 11353, Applisequence 11354, Applisequence 1
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Sequence 151016,
Sequence 17618, A
Sequence 151016,
Sequence 8213, Ap
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Sequence 30378, P
Sequence 6627, Ap
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Patent No. US20020165346A1
Patent No. US20020165346A1
FARENCE INFORMATION:
APPLICANT: Schering-Plough Corporation
TITLE OF INVENTION: MAMMALIAN MEMBRANE PROTEIN GENES; RELATED REAGENTS
FILE REFERENCE: SP0695B
CURRENT PAPLICATION NUMBER: US/09/862,802
CURRENT FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US/09/862,802
CURRENT FILING DATE: 1998-07-08
NUMBER OF SEQ ID NOS: 11
SOSTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
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COTHER INFORMATION: mammalian nucleic acid
NAME/KEY: CDS
LOCATION: 257...1204
OTHER INFORMATION: protein coding sequence
NAME/KEY: variation
LOCATION: 608...673
COCATION: Short form lacks these nucleotides
US-09-862-802-3
                  7 US-10-30S-720-1186

WYS-10-236-392-9

US-09-880-107-2335

US-09-880-107-2235

US-09-980-107-235

US-09-918-95-8784

US-09-918-95-8784

US-09-918-95-8784

US-09-918-95-8784

US-09-917-800A-1642

US-09-917-800A-1642

US-09-917-800A-1642

US-10-052-6-84-46

US-10-926-684-49

US-10-926-684-51

US-10-170-097-49

US-10-170-097-49

US-10-170-097-49

US-10-170-097-51

US-10-027-632-11518

US-10-027-632-17618

US-09-960-352-11618

US-09-960-352-11618

US-09-960-352-17618

US-09-918-995-8213

US-09-918-995-31378

US-09-918-995-31378

US-09-918-995-31378
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100.0%; Score 1458;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1458; Conservative 0; Mismatches
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225.2
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ORGANISM: Unknown
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LENGTH: 1458
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Sequence 45, Appli
Sequence 45, Appl
Sequence 492, Appl
Sequence 9, Appli
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Sequence 89, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 87, Appl
Sequence 1777, App
                                                                                                                                                                                                    (without alignments)
9708.761 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | / Ggn2_6/ptodata/2/pubpna/US07_PUBCOMB. Beq:*
| / Ggn2_6/ptodata/2/pubpna/US07_NEW_PUB. seq:*
| / Ggn2_6/ptodata/2/pubpna/US06_NEW_PUB. seq:*
| / Ggn2_6/ptodata/2/pubpna/US06_PUBCOMB. seq:*
| / Ggn2_6/ptodata/2/pubpna/US06_PUBCOMB. seq:*
| / Ggn2_6/ptodata/2/pubpna/US08_PUBCOMB. seq:*
| / Ggn2_6/ptodata/2/pubpna/US08_PUBCOMB. seq:*
| / Ggn2_6/ptodata/2/pubpna/US08_PUBCOMB. seq:*
| / Ggn2_6/ptodata/2/pubpna/US09_PUBCOMB. seq:*
| / Ggn2_6/ptodata/2/pubpna/US10P_PUBCOMB. seq:*
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                                                                                                                                                                            May 27, 2005, 22:27:31 ; Search time 922 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-925-302-18
VS-10-138-588-87
US-10-152-319A-1777
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US-09-728-952-45
0 US-09-960-706-492
US-09-862-802-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-829-107-9
US-10-138-588-89
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                         nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Score

Result

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FEATURE:
NAME/KEY: misc_feature
LOCATION: (1064)...(1064)
OTHER INFORMATION: nucleotide 1064 of DCMP2s may be A, which would encode Asn rather
OTHER INFORMATION: than Asp at the residue numbered 270
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APPLICANT: Ravel, Odile
APPLICANT: Bates, Elizabeth Ester Mary
APPLICANT: Bates, Elizabeth Ester Mary
APPLICANT: Bates, Elizabeth Ester Mary
APPLICANT: Ford, John
APPLICANT: Lebecque, Serge J.E.
APPLICANT: Lebecque, Serge J.E.
APPLICANT: Saeland, Sem
; TITLE OF INVENTION: Isolated Mammalian Membrane Protein Genes; Related Reagents
; TITLE OF INVENTION: 180104-04-21
CURRENT APPLICATION NUMBER: US/09/862,802A
FRIOR FILING DATE: 2001-05-22
PRIOR FILING DATE: 1997-07-09
; PRIOR FILING DATE: 1997-07-09
; PRIOR FILING DATE: 1998-07-08
; WHORE RO SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
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                                           1381 AGCTTTTATTTTTTTCCAACTTTTGAAAGTCAACTTCATGAAGGTATAATTTTTTACATA 1440
                    AGCTITIATITITITICCAACTITIGAAAGTCAACTICAIGAAGGIATAAATTITIACATA 1440
                                                                                                  TCACTGAGCTGCCTTTGGTGGGACCACCGGCCACAGAAATGGCGGTGGGAGGACTC
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NAME/KRY: misc_feature
LOCATION: (608)..(673)
OTHER INFORMATION: short form lacks nucleotides 608-673
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NAME/KEY: CDS
LOCATION: (257)..(1204)
OTHER INFORMATION: protein coding sequence
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LOCATION: (775)...(776)
OTHER INFORMATION: ASGERM (Table 2)
OTHER INFORMATION: ides 775-776
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; Publication No. US20040192892A1
; GENERAL INFORMATION:
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ORGANISM: Unknown
FEATURE:
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US-10-829-107-3
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                                                                                                                                                                                                                                                                                                                                                                 GAAAGTCCAGGGGTTTAAAAATGGGCCACTTCCTCTCCAGTCCCTCCTGCAGCGTCTCCG 360
1 GTTGAGGAGATGTCCCAGATGATAGGGCTCCTGGGATTTCAGACCCAAGACCAGG 60
                                                        61 AGGACTCCAGTCACCTCTACCCCAGCTCTCCAGGACACAGGGCTCCCAACTCTGAGTGAC
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                                     AGGACTCCAGTCACCTCTACCCCAGGACACAGGGCTCCCCAACTCTGAGTGAC
                                                                                                                     GTCCCACCTCTGGTCCTTGCAGCAAACGTGGGGAATCACACCCTCCAGACCTCCCA
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APPLICANT: Tang, Y. Tom
APPLICANT: Shou, Ping
APPLICANT: Chou, Ping
APPLICANT: Goodfich, Ryle
APPLICANT: Goodfich, Ryle
APPLICANT: Mang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Yamazaki, Vicki
APPLICANT: Yamazaki, Vicki
APPLICANT: Yamazaki, Vicki
APPLICANT: Wang, Dumanac, Radoje T.
TITLE OF INVENTION: No. US20020111302A1e1 Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 79
CURRENT APPLICATION NUMBER: US/09/728,952
CURRENT FILING DATE: 2000-11-30
NUMBER OF SEQ ID NOS: 101
SOGTWARE: PL FL genes Version 2.0
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98.4%; Score 1434.2;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1455; Conservative 0; Mismatches
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; Patent No. US20020111302A1
; GENERAL INFORMATION:
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, LOCATION: (397)..(1356)
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	REBUILT. US-500-560-706-492 Sequence 492 Publication Wo USZ000314280A1 Sequence 492 Publication Wo USZ000314280A1 TITLE OF INVENTION: dentifying Drugs for and Diagnosis of Benign Prostatic Hyperplass TITLE OF INVENTION: dentifying Drugs for and Diagnosis of Benign Prostatic Hyperplass TITLE OF INVENTION: dentifying Drugs For and Diagnosis of Benign Prostatic Hyperplass TITLE OF INVENTION: dentifying Drugs For and Diagnosis of Benign Prostatic Hyperplass TITLE OF INVENTION: dentifying Drugs Prostatic APPLICATION NUMBER: 1031-09-24 PRIOR APPLICATION NUMBER: 1031-09-24 PRIOR APPLICATION NUMBER: 05/873.313 PRIOR APPLICATION NUMBER: 05/873.313 PRIOR APPLICATION NUMBER: 05/873.319 PRIOR APPLICATION NUM
61 AGGACTCCAGTCACCTCTACCCCAGCTCTCCAGGACACAGCGCTCCCAACTCTCAGTGAC 120 201 AGGACTCCAGTCACCTCTACCCCAGCTCTCCAGGACACACCCCCAACTCTCAGTGAC 260 121 GTCCCACTCTCTCTCACCCCAGCTCTCCAGGACACCTCCCAACTCTCAGTGAC 260 121 GTCCCACCTCTGGACACACACCACCTGCGAATCACACCTCCCAACTCTCAGACTCCCA 320 181 CAGCTCCACCTCTGCAGCACAACCACCTCCATTCAGCTGTGACACTCCCAGACTCCCA 320 181 CAGCTCCACCTCTGCAGCACAACCACCTCCATTCAGCTGTGACACCTCCAGA 380 241 CAGCTCCACCCCAGCATGAAACACACCTCCATTTCAGCTGTGACAACTCAGAG 380 241 CCGTGTTGGCCCAAGCATGAAACACGCCTGCCTCCATTTCAGCTGTACACACCTCAGAG 380 241 CCGTGTTGGCCCAAGCATGAAACAGACGTTCCATTTCAGTACTTTGAAAATAAGGT 440 381 CCGTGTTGGCCCAAGCATGAAACAGACTTCCTCTCCAGTACTTTGAAAATAAGGT 440 381 CCGTGTTGGCCCAAGCATGAAAGACTTCCTCTCCAGTACTTTGAAAAATAAGGT 440 381 CCGTGTTGGCCCAAGCATGAAAGACTTCCTCCAGTACTTTGAAGAATAAAGT 420 11	121 CTGTGTGGTTGGATTCGAAATTCGAAATTTCAGAGGGCTCGTGACCTGGGACAGA 180 181

DD 1300 GAAGGTATTATACATAATAAAAATGCACTCATTT 1337	RESULT 5 US-09-862-802-9 ; Sequence 9, Application US/09862802 ; Patent No. US20020165346A1 ; GENERAL INFORMATION: ; APPLICANT: Schering-Plough Corporation ; TITLE OF INVENTION: MAMMALIAN MEMBRANE PROTEIN GENES; RELATED REAGENTS	/09/862,8 10 9/111,470		; OTHER INFORMATION: mammalian nucleic acid ; NAME/KEY: CDS ; LOCATION: 2731091 ; OTHER INFORMATION: protein coding sequence US-09-862-802-9	Query Match 76.0%; Score 1108; DB 9; Length 1370; Best Local Similarity 89.4%; Pred. No. 2.6e-297; Matches 1288; Conservative 0; Mismatches 5; Indels 147; Gaps 3; Qy 28 TAGGGCTCCTGGGATTTCAGACCCAAGACCAGGCAGCTCTACCCCCAGCT 87	44 TACTGTCCCTGGGATTTCAGATCCAAGACCAGCAGCTCCAGTCACTCTACCCCAGCT 88 CTCCAGGACACACGCTCCCAACACACAAA	DB 104 CTCCAGGACACACCCTCCCAACTCTGAGTGACGTCCCACCTCTGGTCCTTGCAGCACAA 163 Qy 148 CCAACGTGGGAATCACACCTCCAGACCTCCCACAGCTCCACACTGGGGCGCGGC 207	208 CCTGCCTCCATTTCGCTGTGACAACCTCAGAGGGTTTGGCCCAAGCATGACAAGGAC 224 CCTGCCTCCATTTCAGCTGTGACAACCTCAGAGGACGTGTTGGCCCAAGCATGACAAGGACAAGGACAAGGACGAGGACGAGGACGAGGACGAGGACGAGGACGAGGACGAGGACGAGGACGAGGACGAGGACGAGGACGAGGACGAGGACGAGGACGAGGACGAGGACGAGGACGAGGACGAGGACAAGGACGAC	268 GTATGAAAACTTCCAGTACTTGGAGAATAAGGTGAAAAGTCCAGGGGTTTAAAAATGGGC 	328 ACTTCCTCTCCAGTCCTCTGCAGCGTCTCCGCTCTGGGCCCTGCCATCTCCTGCTGTC	388 CCTGGGCCTGCTGCTGGTCATCATCTGTGTGGTTGGATTCCAAATTCCAA [448 ATTTCAGAGGACCTGGTGACCTGAGAACAGATTTAGCAACTTCACCTCAAACAGTTTAGCAACTTCACCTCAAACAGTTTAGCAACTTCACCTCAAACACTGTTTTAGCAACTTCACCTCAAACACTTCAAACACTTCAAACACTTCAAACACTTCAAACACTTCAAACACTTCAAACAAC	#07 AIIICAGAGGACCIGGIGACCCCIGAGGAGAIIITAGCAATIICAACIICAACAGGG 508 GGCGGAGATCCAGGCACTGCCAGGCAGCAGCTTGGAAGAACGATAGCATCTCT	568 GAAAGCTGAGGTGGGAGGTTTCAAGCAGGAACGGCAGGGGGTATCTGAGCTCCAGGA
350 CAGGGTCTCGGCTCTGGGCCCTGCCTGCTGTCCTGGGGCCTGGGCTGCT	410 CTGGTCATCTGTGTGGTTGCAAAATTCCAAATTTCAGAGGGCCTGGTGACC 469	TCCCAGGGCAGCTGGAAGAAACGATAGCATCTCTGAAAGCTGAGGTGGAGGCTTTC		710 CGAGTCCAGCAGCTGGTGCAAGACCTGAAAAACTGACCTGCCAGGTGGCTACTCTCAAC 769		100 CAAGACAGCTGCTACTGGTTCTCTCACTCTGGGATGTCCTGGGCCGAGGCTGAGAAGTAC 759 881 TGCCAGCTGAAGAACGCCCACCTGGTGGTCATCAACTCCAGGAGGAGGAGCAGAATTTTGTC 940 160 TGCCAGCTGAAGAACGCCCACCTGGTGGTCATCAACTCCAGGGAGGAGCAGAATTTTGTC 819	941 CAGAAATATCTAGGCTCCGCATACACCTGGATGGCCCTCAGTGACCCTGAAGGAGCCTGG 1000 	1001 AAGTGGGTGGATGGAACAGACTATGCGACCGGCTTCCAGAACTGGAAGCCAGGCCAGCCA	1061 GACGACTGGCAGGGCACGGCTGGGTGGGAGGACTGTGCTCATCCATC		1181 GGTCAGACCAGGAGAGTCACTGAGCTGCCTTTGGTGGGACCACCCGGCCACAGAAA 1240 	1241 TGGCGGTGGGAGGACTCTTCTCACGACCTCCTCGCAAGACCGCTCTGGGAGAGAAT 1300 	1301 AACCACTGGGAGATTGGAAGCACTGCTAACATTTTGAATTTTTTCTCTTTAATTTTAAA 1360 	1361 AAGAIGGTATAGIGTICTTAAGCTTTTATTTTTTCCAACTTTGAAGTCAACTTCAT 1420

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                                                                                                                                                                                                                                                                             Length 1370;
                                                                                                                                TYPE: DNA
ORGANISM: Unknown
PERJURE:
OTHER INFORMATION: mammalian nucleic acid and protein
                                                                                                                                                                                                                                                                            Query Match 76.0%; Score 1108; DB 18;
Best Local Similarity 89.4%; Pred. No. 2.6e-297;
Matches 1288; Conservative 0; Mismatches 5;
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                                                                                                                                                                                       FEATURE:
NAME/KEY: CDS
LOCATION: (273)..(1091)
OTHER INFORMATION: protein coding sequence
US-10-829-107-9
                60/053,080
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 1997-07-09
PRIOR APPLICATION NUMBER: US 09/;
PRIOR FILING DATE: 1998-07-08
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 9
LENGTH: 1370
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Publication No. US20040192892A1
Publication No. US20040192892A1
Publication No. US20040192892A1
APPLICANT: Valladeau, Jenny
APPLICANT: Ravel, Odile
APPLICANT: Bates, Elizabeth Ester Mary
APPLICANT: Ford, John
APPLICANT: Lebecque, Sem
TITLE OF INVENTION: Isolated Mammalian Membrane Protein Genes; Related Reagents
FILE REFERENCE: SF0695 B
FILE REFERENCE: SF0695 B
FILE REFERENCE: ST04-04-21
CURRENT FILING DATE: 2004-04-21
PRIOR APPLICATION NUMBER: US/09/862,802A
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                                                                     DB 17; Length 1072;
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                                                                  Score 1039.2; DB 1'
Pred. No. 3.2e-278;
0; Mismatches 3;
                                                                   71.3%;
Similarity 98.9%;
50; Conservative (
 ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (45)..(1002)
US-10-138-588-89
                                                                                Best Local Sim:
Matches 1060;
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JAPPLICANT: ALSODEON ET AL.

TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES, NUCLEIC ACT
TITLE OF INVENTION: ENCOING THE ANTIGENS, AND METHODS OF USE
FILE REFERENCE: 21402-347A

CURRENT APPLICATION NUMBER: US/10/138,588

CURRENT FILING DATE: 2002-05-01

PRIOR APPLICATION NUMBER: 60/288,395

PRIOR FILING DATE: 2001-05-03

PRIOR FILING DATE: 2001-05-03

PRIOR FILING DATE: 2001-08-17

PRIOR PLLING DATE: 2001-08-17

PRIOR APPLICATION NUMBER: 60/324,757

PRIOR PLLING DATE: 2001-08-17

PRIOR PILING DATE: 2001-08-17

PRIOR PILING DATE: 2001-08-17

PRIOR FILING DATE: 2001-08-17

PRIOR FILING DATE: 2001-08-17

PRIOR FILING DATE: 2001-08-18

SEQ ID NO 89

LENGTH: 1072

TWOEL NAME
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                                                                              CAGGGAGGAGCAGAATTTTGTCCAGAATATCTAGGCTCCGCATACACCCTGGATGGGCCT
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ORGANISM: Homo sapiens
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REPERENCE: PA104
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 18
LENGTH: 929
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OTHER INFORMATION: n equals a,t,g, or
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LOCATION: (431)
OTHER INFORMATION: n equals a,t,g, o
NAME/KEY: misc feature
LOCATION: (613)
OTHER INFORMATION: n equals a,t,g, o
NAME/KEY: misc feature
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NAME/KEY: misc feature
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ORGANISM: Homo sapiens
FEATURE:
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US-09-925-302-18
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                            961 TCTGCGAGGCTGGCCTGGGTCAGACCAGCAGAGAGAGTCACTGAGCTGCCTTTGGTGGGA
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                                                                                                                1021 CCACCCGGCCACAGAAATGGCGGTGGGAGGAGGAGTCTTCTCACGACCTCCT 1072
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Patent No. US20020044941A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA104

CURRENT APPLICATION NUMBER: US/09/925,302

CURRENT FILING DATE: 2001-08-10

PRIOR PILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR PILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 896

SOFTWARE: PATENT VET. 1999-03-12

NUMBER OF SEQ ID NOS: 896
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49.7%; Score 724.2; DB 9;
Best Local Similarity 89.8%; Pred. No. 1.4e-190;
Matches 836; Conservative 6; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: (613)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (918)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (929)
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OTHER INFORMATION: n equals a,t,g, or
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US-09-925-302-18
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LENGTH: 929
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Sequence 87, Application US/10138588
Publication No. US20040018594A1
GENERAL INFORMATION:
APPLICANT: Alsobrook et al.
ITILE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES, NUCLEIC ACII;
ITILE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
FILE REFERENCE: 21402-3478; US/10/138,588
CURRENT FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: 60/288,395
PRIOR FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: 60/308,901
PRIOR PLING DATE: 2001-08-17
PRIOR PLING DATE: 2001-08-17
PRIOR PLING DATE: 2001-09-25
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 203
SEQ ID NO 87
LENGTH: 820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 714.6; DB 17;
Pred. No. 6.1e-188;
0; Mismatches 9;
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Best Local Similarity 90.0%;
Matches 811; Conservative
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ORGANISM: Homo sapiens
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; LOCATION: (3)..(804)
US-10-138-588-87
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                                                                                                                                                                                                                                                  92 AGGACTCCAGTCACCTCTACCCCAGCTCTCCAGGACACAGGGCTCCCAAGTGAC 151
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                                                                                               Gaps
                                                                                            83;
                                                      Length 929
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                                                    DB 10;
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                                               Query Match 49.7%; Score 724.2; DB 10
Best Local Similarity 89.8%; Pred. No. 1.4e-190;
Matches 836; Conservative 6; Mismatches 6;
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0; Mismatches 295; Indels
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| Gequence 1777, Application US/10152319A
| GENERAL INFORMATION:
| Gequence 1777, Application US/10152319A
| GENERAL INFORMATION:
| APPLICANT: Monson, Kory
| APPLICANT: Higgs, Brandon
| APPLICANT: Castle, Arthur
| APPLICANT: Castle, Arthur
| APPLICANT: Castle, Arthur
| APPLICANT: Elashoff, Michael
| TITLE OF INVENTION: Molecular Toxicology Modeling
| FILE REFERENCE: 44921-5089-US
| TITLE OF INVENTION NUMBER: US 60/29; 335
| FRIOR FILING DATE: 2002-05-22
| PRIOR FILING DATE: 2001-06-13
| PRIOR FILING DATE: 2001-06-13
| PRIOR FILING DATE: 2001-06-13
| PRIOR FILING DATE: 2001-07-10
| PRIOR F
                          520 GGGAGGAGAATTTTGTCCAGAAATATCTAGGCTCCGCATACACCTGGATGGGCCTCA
                                                                                                                  580 GTGACCCTGAAGGAGCCTGGAAGTGGGTGGGAACAGACTATGCGACCGGCTTCCAGA
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GGGAGGAGAGTTTTGTCCAGAAATATCTAGGCTCCGCATACACCTGGATGGGCCTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE: OTHER INFORMATION: Genbank Accession No. NM_022393
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ORGANISM: Rattus norvegicus
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Best Local Similarity
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US-10-152-319A-1777
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Sequence 1186, Application US/10305720

Publication No. US20040010136A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression;
FILE REFERENCE: PA-0002-1 CON
CURRENT APPLICATION NUMBER: US/10/305,720
CURRENT FILING DATE: 2002-11-26
PRIOR FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 1490
SOFTWARE: PERL Program
SEQ ID NO 1186
LENGTH: 1277
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                                                                                           716 TGCCGGCTGGACGACGCGCACCTGGTGGTCACGTCCTGGGAGGAGGAGAATTTGTC
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66.1%; Pred. No. 3e-95;
ive 0; Mismatches 245; Indels 87
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ORGANISM: Homo sapiens
PEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: GenBank ID No. US20040010136A1 g179078
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Matches 646; Conservative
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US-10-305-720-1186
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                                                                                                                  APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scharf, Uwe
APPLICANT: Scharf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer;
FILE REFRENCE: 4421-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT PILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
FRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/217,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3350
SOFTWARR: PALENTIN Ver. 2.1
SEQ ID NO 2230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 M10058
US-09-880-107-2230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 382; DB 9; Length 1277;
Pred. No. 3e-95;
0; Mismatches 245; Indels 8
Sequence 2230, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
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Best Local Similarity 66.1%;
Matches 646; Conservative
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APPLICANT: Pewman, John A

APPLICANT: Pewman, John A

APPLICANT: Rester! Daniel K

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APPLICANT: Shinkee's Richard A

TITLE OF INVENTION THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME

FILE REFERENCE: 2140-442A

CURRENT FILING DATE: 2002-09-00

PRIOR PPLICATION NUMBER: US60/390,155

PRIOR PLING DATE: 2000-08-10

PRIOR PLING DATE: 2000-09-10

PRIOR PLING DATE: 2000-09-07

PRIOR PLING DATE: 2000-09-07

PRIOR PLING DATE: 2001-09-07

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       308 CAGGGGTTTAAAAAATGGGCCACTTCCTCTCCCAGTCCCTCCTGCAGCGTCTCCGCTCTGGG
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     Padigaru, Muralidhara
                                  Patturajan, Meera
Pena, Carol A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 62.1
Matches 591, Conservative
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; LOCATION: (121)..(982)
US-10-236-392-9
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440 GGCTTGAGCACCCCAGGGAGGCAATGTGGGAAGAAGATGAAGTCGCTAGAGTCCCAGCTG 499
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                                                                                   GAGGGTTTCAAGCAGGAACGGCAGGCAGGGTATCTGAGCTCCAGGAACACACTACGCAG
                                                                                                                                       Sequence 9, Application US/10236392; Publication Wo. US20040067490A1; Publication No. US20040067490A1; APPLICANT: Anderson, David WAPPLICANT: Boldog, Ferenc LAPPLICANT: Boldog, Ferenc LAPPLICANT: Casman, Stacie J
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Gerlach, Valerie
Gorman, Linda
Grosse, William M
Gusev, Vladamir
Kekuda, Ramesh
LaRochelle, William J
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Chapoval, Andrei
Crabtree, Julie
Edinger, Shlomit, R
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Malyankar, Uriel M
Miller, Charles E
Millet, Isabelle
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        GGGACCTGCTCCCCGTCAACTGGGTGGAGCACCAAGACAGCTGCTACTCTCTCAC
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        568
        AGGACCTGCTGCCCCGTCAACTGGAGCACCAAGGCAGCTGCTACTGGTTCTCTCAC
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                                              TGCCCATCTGTGTGTCCCAGTTCATTCTGAAATGCTCCTGCGAGTCCAGCAGCTGGTG 727
                                                                                                               511 GIGGACCTGCGCTTCGTGGCCTGCCAGATGGAGCTCCTCCACAGCAACGCTCC---CAA
GGGGTATCTGAGCTCCAGGAACACACTACGCAGAAGGCACCCTAGGCCCACTGTCCCCAC
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Sequence 3731, Application US/09880107

Sequence 3731, Application US/09880107

GENERAL INFORMATION:

APPLICANT: Horne, Darci T.

APPLICANT: Scherf, Uwe

APPLICANT: Gene Logic, Inc.

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer;

FILE REFERENCE: 44921-5028-WO

CURRENT FILING DATE: 2001-06-14

PRIOR APPLICATION NUMBER: US 60/211,379

PRIOR APPLICATION NUMBER: US 60/211,379

PRIOR PILING DATE: 2000-10-02

PRIOR PILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 3950

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 3731

LENGTH. 1300
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US-09-880-107-3731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22.0%; Score 321.4; DB 9; Length 1300; 62.1%; Pred. No. 2.2e-78; ive 0; Mismatches 276; Indels 84;
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Matches 591; Conservative
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ORGANISM: Homo sapiens
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## ALIGNMENTS

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3 S	<pre>C-type lectin, superramily member 13, Name=CLECSF14;</pre>	, superramı ;	Ty me	moer 13	18	IBOLOKH 1.	
SO	Homo sapiens (Human)					,	
႘ၟၟ	Eukaryota, Metazoa, Mammalia, Eutheria,		Chordata;		ta; hini	Craniata; Vertebrata; Butele Catarrhini: Hominidae: Homo	Craniata; Vertebrata; Euteleostomi; Catarrhini: Hominidae: Homo
88	NCBI TaxID=9606;	š				,	
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RP	SEQUENCE FROM N.A.	N.A.					
<u>ي</u>	TISSUE=Brain;			0	,		
ž	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899 Stransberg D T. Reingold R A Gronse T. H. Derge J G	257; Pubmed	124 P	1932; D	01=10 86 -1	0.1073/pnas.	242603899;
\$ &	Klansner R.D.	Collins F	, ,	Wagner	ָ	Shenmen C.M.	Schuler G.D.
æ	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat	Zeeberg B	 B	etow K.	H	Schaefer C.F	Z
Æ	Hopkins R.F.,	Jordan H.,	Moor	e T., M	ax S	.I., Wang J.	124
RA.	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	, Marusina	К.,	armer A	A.	Rubin G.M.,	Hong L.,
RA:	Stapleton M.,	Soares M.B	 	naldo M	1	. Casavant T.	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
<b>\$</b> £	Brownstein M.J., Usdin T.B.,	r usair	n s	ortneor.	or in	, Carninci	F., Frange C.,
5 5	Bosak S.A. Mo	Ewan P.J.	MCKe	rnan K.		Malek J.A.	Gunarathe P.H.
8	Richards S., W	Worley K.C.	Hal	e S.	arci	a A.M., Gay	L.J., Hulyk S.W.,
æ	Villalon D.K.,	Muzny D.M	., S	dergren	E.C	., Lu X., Gi	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
8 2	Fahey J., Helt	con E., Ket	temar	Ma	dan	A., Rodrigue	ss S., Sanchez A.,
<b>5</b> 6	MILLING M., Md	Touchman	511	7.C., 31	) ) )	CILKO I., BOU	1.5.6 G.G.,
§ §	Rodriquez A.C.	., Grimwood		Schmutz		Myers R.M.,	BlakeBiey N.M., Jouchman J.M., Green B.D., DickBun M.C., Rodriquez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA	Krzywinski M.1	I., Skalska	, U.,	Smailue	Ω.	., Schnerch	A., Schein J.E.,
RA	Jones S.J., Ma	arra M.A.;					
RT	"Generation an	nd initial	anal)	rais of	шore	than 15,000	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences.";	A sequences			00-1	(2002) 50031-00031-00	
Z Z	[2]	, dd			1	. (2002) 5050	
RP	SEQUENCE FROM N.A	N.A.					
RC	TISSUE=Brain;						
Z.	Strausberg R.;				•		
3	Submitted (NOV-2002) to the	7-2002) to		MBL/Gen	Bank	EMBL/GenBank/DDBJ databases	ıses.
H I	EMBL, BC039011; AAH39011.1;	1; AAH39011					
¥ 6	HSSP; P07306; IDV8.	IDVB.	4.14				
š 6	GO: GO: 0016020	O. C. membra		43			
S S	GO; GO:0005529; F:sugar binding;	9; F:Bugar	bind	ng; IEA	:		
DR	InterPro; IPR002353; Antifreezell	002353; Ant	ifre	zell.			•
D.	InterPro; IPRO	IPR001304; Lec	Lectin_C.	.;			
ਲ (	InterPro; IPRO	005640; lec	tin	_:			
R I	Pfam, PF00059; Lectin_C; 1.	Lectin C;	႕,				
g i	Ptam; PF03954;	Lectin N;	1.				
ž 5	PKINTS; PKUU356; ANTIFKEEZEII SMART: SM00034; CLECT: 1.	be; ANTIFRE	EZEL	:			

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MEDINE-223825; PubMed=12477932; DOI=10.1073/pnas.242603899; MEDINE-223825; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F., Diatchenko L., Marusina K., Paramer A.A., Rubin G.M., Hong L., Stapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheez T.E., Bronstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Araba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Allalon D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A., Willalon D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Antering M., Touchman J.W., Green E.D., Dickson M.C., Antering M. Salska M.J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Marra M.A., Touchman M., Modes S.J., Marra M.A., Touchman M., Sonmutz J., Myers R.M., Schein J.E., Marra M.A., Touchman J.W., Geen E.D., Dickson M.C., Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                     ONSKFORDLVTLRTDFSNFTSNTVAEIQALTSQGSSLEETIASLKAEVEGFKQERQAGVS 120
                                                                                                                                                                   ONSKFORDLVTLRTDFSNFTSNTVAEIOALTSOGSSLEETIASLKAEVEGFKOEROA--- 117
                                                                                                                                                                                                                                               121 ELQEHTTQKAHLGHCPHCPSVCVPVHSEMLLRVQQLVQDLKKLTCQVATLNNN---ASTE 177
                                                                                                                                                                                                                                                                                                                                                                                               154 GTCCPVNWVEHQDSCYWFSHSGMSWAEAEKYCQLKNAHLVVINSREEQNFVQKYLGSAYT 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 -----VHSEMLLRVQQLVQDLKKLTCQVATLNNNGEEASTE 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               WMGLSDPEGAWKWVDGTDYATGFQNWKPGQPDDWQGHGLGGGGEDCAHFHPDGRWNDDVCQ 297
                              MTRTYENFOYLENKVKVQGFKNGPLPLQSLLQRLRSGPCHLLLSLGLGLLLLVIICVVGF
                                                             1 MTRIYENFQYLENKVKVQGFKNGPLPLQSLLQRLRSGPCHLLLSLGLGLLLLVIICVVGF
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Name=CLECSF14;
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MEDLINE=96108853; PubMed=8598452;
Suzuki N., Yamamncor K., Toyoshima S., Osawa T., Irimura T.;
"Molecular cloning and expression of cDNA encoding human macrophage type lectin: Its unique carbohydrate binding specificity for Tn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 7.3e-121;
0; Mismatches 0;
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J. Immunol. 156:128-135(1996).
EMBL; D950532; BA409101.1; --
HSEP; P07306; 1DV8.
GO; GO:0005886; C:plasma membrane; TA:
GO; GO:0005529; F:sugar binding; TAS.
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Pfam; PF01954; Lectin N; 1.
PRINTS, PR00136; ANTIFREEZEII.
SMART; SM00034; CIECT; 1.
PROSITE; PS00615; C TYPE LECTIN 1; 1.
PROSITE; PS50041; C TYPE LECTIN 1; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1. PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
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InterPro; IPR001304; Lectin C.
InterPro; IPR005640; lectin N.
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Best Local Similarity 90.6%;
Matches 289; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max. S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
                                                                                                            1 MTRIYENFQYLENKVKVQGFKNGPLPLQSLLQRLRSGPCHLLLSLGLGLLLLVIICVVGF
                                                                                                                                  MTRIYENFOYLENKVKVQGFKNGPLPLQSLLQRLRSGPCHLLLSLGLGLLLLVIICVVGF
                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1988 (Rel. 07, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Asialoglycoprotein receptor 1 (Hepatic lectin H1) (ASGPR) (ASGP-R)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Mang H., Gao X., Li L., Lou H., Huang Y., Wang B., Han J.,

"Human asialoglycoprotein receptor 1 gene is expressed in SH-SYSY
human neuroblastoma cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=85130911; PubMed=2982798; Spiess M., Schwartz A.L., Lodish H.F.; Sequence of human asialoglycoprotein receptor cDNA. An internal signal sequence for membrane insertion."; Biol. Chem. 260:1979-1982(1985).
                                                                                     27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Liver;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnss.242603899;
                                                           57.5%; Score 998.5; DB 2; Length 256; 87.6%; Pred. No. 2.7e-75; ive 1; Mismatches 0; Indels 27.
                                                                                                                                                                                                                                                            CPVNWVEHQDSCYWFSHSGMSWAEAEKYCQLKNAHLVVINSREG 225
                                                                                                                                                                                                                                                                          to the EMBL/GenBank/DDBJ databases.
                                      C2C1A576F369647D CRC64;
                                                                                                                                                                                                                                                                                                                                                290 AA.
     01-APR-1988 (Rel. 07, Created)
InterPro; IPR005640; lectin_N.
                                                                        Best Local Similarity 87.6
Matches 197; Conservative
                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell 44:177-185(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (SEP-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                         Name=ASGR1;
                                                                                                                                                                                                                                                                                                                                                LECH HUMAN
P07306;
                                                                                                                                                                                                                                    118
                                                                                                                                                                                                                                                            181
                                                                                                                                                            61
                                                              Query Match
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones J.M., Marra M.A., Schein J.M., Marra M.A., Schein J.M., Marra M.A., Schein J.M., Marra M.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: Mediates the endocytosis of plasma glycoproteins to which the terminal stalic acid residue on their complex carbohydrate moieties has been removed. The receptor recognizes terminal galactose and N-acetylgalactosamine units. After ligand binding to the receptor, the resulting complex is internalized and transported to a sorting organelle, where receptor and ligand are disassociated. The receptor then returns to the cell membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- SUBCELLULAR LOCATION: Type II membrane protein.
-i- TISSUE SPECIFICITY: Expressed exclusively in hepatic parenchymal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gu K.T., Zhou X.-M., Jiang H.-Q., Zhang P.-P., Huang Y., Li Y.-Y., Gu J.-R., "Cloning, mapping, and characterization of a human homologue of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=11543633; DOI=10.1006/geno.2001.6614;
Pan H., Qin W.-X., Huo K.-K., Wan D.-F., Yu Y., Xu Z.-G., Hu Q.-D., Gu K.T., Zhou X.-M., Jiang H.-Q., Zhang P.-P., Huang Y., Li Y.-Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal-anchor for type II membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C-type lectin.
Endocytosis signal (Potential).
By similarity.
By similarity.
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GO: GO:0004873; F:asialoglycoprotein receptor activity; TAS.
GO: GO:0004898; P:receptor mediated endocytosis; TAS.
InterPro; IPR001304; Lectin_C.
InterPro; IPR00540; lectin_N.
Pfam; PF00159; Lectin_N.
Pfam; PF00159; Lectin_N.
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-!- MISCELLANEOUS: Calcium is required for ligand binding.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
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PROSITE; PSO0615; C_TYPE_LECTIN 1; 1.
PROSITE; PSS0041; C_TYPE_LECTIN 2; 1.
BROSITE; PSS0041; C_TYPE_LECTIN 2; 1.
PROSITE; PSS0041; C_TYPE_LECTIN 2; 1.
Phosphorylation; Receptor; Signal-anchor; Transmembrane.
INIT_MET 1 39 Cytoplasmic (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein (Probable).
Extracellular (Probable)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            yeast longevity assurance gene LAG1.";
Genomics 77:58-64(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: Interacts with LASS2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB070933; BAB83508.1; -. EMBL; BC032130; AAH32130.1; -.
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PDB; 1DV8; X-ray; A=153-280.
Genew; HGNC:742; ASGR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M10058; AAA51785.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [5]
INTERACTION WITH LASS2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39
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153
181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 QNSQLRRDLETLRTTLDNTTSNTKAELQALASRGDSLQTGINSLKVEVDDHGQELQAGRG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 ----VSELQ-----EHTTQKAHLGHCPHCPSVCVPVHSEMLLRVQQLVQDLKKLTCQVAT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 QNSKFQRDLVTLRTDFSNFTSNTVAEIQALTSQGSSLEETIASLKAEVEGFKQERQAG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 LSQKVASLESTVEKKEQTLRTDL------SEITDRVQQLGKDLKTLTCQLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LINNIASTEGICCPVNWVEHQDSCYWFSHSGMSWAEAEKYCQLKNAHLVVINSREEQNFVQ
  Ii M., Kurata H., Itoh N., Yamashina I., Kawasaki T.;
"Molecular cloning and sequence analysis of cDNA encoding the
macrophage lectin specific for galactose and N-acetylgalactosamine.";
J. Biol. Chem. 265:11295-11298 (1990).
                                                                                                                                          Biochem. Biophys. Res. Commun. 155:720-725(1988).
-!- FUNCTION: Recognizes terminal galactose and N-acetylgalactosamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MTRIYENFQYLENKVKVQGFKNGPLPLQSLLQRLRSGPCHLLLSLGLGLLLLVIICVVGF
                                                               PRELIMINARY SEQUENCE OF 9-28.
MEDLINE-88319956; PubMed=3421964;
MI M., Kawasaki T., Yamashina I.;
"Structural similarity between the macrophage lectin specific for galactose/N-acetylgalactosamine and the hepatic asialoglycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C-type lectin.

By similarity.

By similarity.

By similarity.

N-linked (GlcNAc. ..) (Potential)

N-linked (GlcNAc. ..) (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28;
                                                                                                                                                                                                                                                                                                                               EMBL, J05495; AAA41216.1; -
PIR; A42230, A42230.
HSSP, PO7306, 1DV9.
InterPro; IPR001303; Antifreezell.
InterPro; IPR001304; Lectin C.
InterPro; IPR00540; Lectin C.
InterPro; IPR00563; Prefoldin.
Pfam; PP00059; Lectin C; 1.
Pfam; PR00059; Lectin N; 1.
PRINTS; PR00354; ANTIFREEZEL.
SWART; SM00034; CLECT; 1.
PROSITE; PS000615; CTYPE_LECTIN 1; 1.
PROSITE; PS50041; CTYPE_LECTIN 2; 1.
ROSITE; PS50041; CTYPE_LECTIN 2; 1.
Calcium; Direct profein sequencing; Glycoprotein; Lectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80; Indels
                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: Type II membrane protein.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytoplasmic (Potential).
Signal-anchor for type II protein (Potential).
Extracellular (Potential).
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D68A5DFF0B9E8F13 CRC64;
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54.8%; Pred. No. 7.4e-66;
ive 38; Mismatches 80,
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                                                                                                                               binding protein.";
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   213 LHDQNGPWKWVDGTDYETGFKNWRPEQPDDWYGHGLGGGGEDCAHFTDDGRWNDDVCQRPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1996 (Rel. 33, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Macrophage asialoglycoprotein-binding protein (M-MSGP-BP) (Macrophage agalactose/N-acetylgalactoseamine-specific lectin) (MMGL).
Name=Mgl1; Synonyms-Mgl;
                                                                                                                                                                                                                                                                                                                                                                                               TRIYENFOYLENKVK-VQGFKNGPLPLQSLLQRLRSGPCHLLLSLGLGLLLLVIICVVGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norregicus (Raž).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                       29;
                                                                                                                                                                                                                                                                                                                                             ; Score 918.5; DB 1; Length 290; ; Pred. No. 1.6e-68; 47; Mismatches 67; Indels 29
                                                                                                                                                                                                                                                                                                                       33055 MW; B1897CE30DAE1586 CRC64;
 By similarity.
O-linked.
O-linked.
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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=90293078; PubMed=2358462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1996 (Rel. 33, Created)
                                                                                                                                                                                                                                                                                                                                              52.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             273 RWVCETELDKASÓE 286
                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 54.59
Matches 171; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                  1183
2204
2222
2224
2236
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236
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  DISULFID
CARBOHYD
CARBOHYD
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P49301;
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                                                                                                                                                                                                                                                                                                                     SEQUENCE
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HELIX
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Gaps

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671F043968047DB7 CRC64;

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32591 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            273 RWVCETKLDKAN 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat)
284 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM N.A.
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                                                                                                                                                                                                                                      61
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SEQUENCE
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STRAIN=FVB/N; TISSUE=Liver;

KATAIN=FVB/N; TISSUE=Liver;

KATAIN=FVB/N; TISSUE=Liver;

KATAIN=FVB/N; TISSUE=Liver;

KATAIN=FVB/N; TISSUE=Liver;

KATAIN=FVB/N; Teingold E.A., Grouse L.H., Derge J.G.,

KATAUSHORD R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altachul S.F., Zebeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jozdan H., Moore T., Max S.I., Wang J., Heishe F.,

KATAIN B.F., Jozdan H., Moore T., Max S.I., Wang J., Heishe F.,

Brapheron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garranter P.H.,

Richards S., Worley K.C., Hale S., Garranter P.H.,

Richards S., Worley K.C., Hale S., Garranter B.H.,

Richards S., Worley K.C., Hale S., Garranter B.H.,

Richards S., Worley K.C., Hale S., Garranter G.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
                        Last sequence update)
Last annotation update)
major subunit (Asialoglycoprotein receptor
KYLGSAYTWMGLSDPEGAWKWVDGTDYATGFQNWKPGQPDDWQGHGLGGGGEDCAHFHPDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEGUENCE FROM N.A.
STRAIN=129/SV378-1119(99)00493-X;
STRAIN=129/SV378-1119(99)00493-X;
SOUKHNE-20137499; PubMed=10675034; DOI=10.1016/S0378-1119(99)00493-X;
SOUKHAREV S., Berlin W., Hanover J.A., Bethke B., Sauer B.;
"Organization of the mouse ASGRI gene encoding the major subunit of the hepatic asialoglycoprotein receptor.";
Gene 241:233-240(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AR182811; AAF29495.1; -.
EMBL; BC022106; AAH22106.1; -.
PIR; S29855; S29855.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP, P07306; 1DV8.
MGD; MGI:88081; Asgri.
GO; GO:0016021; C:Integral to membrane; TAS.
GEM: PF00059; Lectin_C; 1.
Pfam; PF03954; Lectin_N; 1.
                                                                                                                                                                                                                                                         284 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PSO0615; C_TYPE_LECTIN_1; 1. PROSITE; PSS0041; C_TYPE_LECTIN_2; 1.
                                                                                          312
                                                                                                                                    284 RWNDDVCQRPYRWVCEMKLAKDS 306
                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                         PRT;
                                                                                          RWNDDVCQRPYHWVCEAGLGQTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00356; ANTIFREEZEII. SMART; SMO0034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19,
25-OCT-2004 (TrEMBLrel. 28,
Asialoglycoprotein receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=FVB/N; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences."
                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                     (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                     01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                        Name=Asgr1;
                                                                                          290
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ONSKFORDLVTLRTDFSNFTSNTVAELQALTSQGSSLEETIASLKAEVEGFKQERQAGVS 120
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                                                                                                                                                                                                                                                                                                                                                                                           240
                                                                                                                                                                                                                                                                                                                        LSDPEGAWKWVDGTDYATGFQNWKPGQPDDWQGHGLGGGGDCAHFHPDGRWNDDVCQRPY 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ONSOLREDILALRONFSNLTVSTEDOVKALSTQGSSVGRKKKTVESKLE--KQQK----
                                                                                                                                                                                                                                                                                                                                                                                                                       1 MTRIYENFQYLENKVKVQGFKNGPLPLQSLLQRLRSGPCHLLLSLGLGLLLLVIICVVGF
                                                                                                                                                                                                                                                                                            121 ELQEHTTQKAHLGHCPHCPSVCVPVHSEMLLRVQQLVQDLKKLTCQVATLNNNASTEGTC
                                                                                                                                                                                                                                                                                                                                                                                           181 CPVNWVEHQDSCYWFSHSGMSWAEAEKYCQLKNAHLVVINSREEQNFVQKYLGSAYTWMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Holland E.C., Leung J.O., Drickamer K.; "Rat liver asialoglycoprotein receptor lacks a cleavable NH2-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kattus nozvejstus (rat.)
Eukaryota; Metazoa (Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                28; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
13-MUG-1987 (Rel. 05, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
Asialoglycoprotein receptor 1 (Hepatic lectin 1) (RHL-1) (ASGP-R)
     Length 284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=86008335; PubMed=2995379;
Leung J.O., Holland B.C., Drickamer K.;
"Characterization of the gene encoding the major rat liver
                                                  Indels
Query Match 50.5%; Score 877; DB 2; L
Best Local Similarity 51.3%; Pred. No. 4.6e-65;
Matches 160; Conservative 54; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    roc. Natl. Acad. Sci. U.S.A. 81:7338-7342(1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      283 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           asialoglycoprotein receptor.";
J. Biol. Chem. 260:12523-12527(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=85063786; Pubmed=6095287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 11-283 FROM N.A.
MEDLINE=87026895; PubMed=2945599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=Asgr1; Synonyms=Asgr-1;
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169 TLINNASTEGICCPVNWVEHQDSCYWFSHSGMSWAEAEKYCQLKNAHLVVINSREEQNFV 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229 QKYLGSAYTWMGLSDPEGAWKWVDGTDYATGFQNWKPGQPDDWQGHGLGGGEDCAHFHPD 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular cloning and characterization of a novel mouse macrophage C-type lectin, mMGL2, which has a distinct carbohydrate specificity from mMGL1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49 LLLLVIICVVGFQNSKFQRDLVTLRTDFSNFTSNTVAEIQALTSQGSSLEETIASLKAEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGFKQERQAGVSELQEHTTQKAHLGHCPHCPSVCVPVHSEMLLRVQQLVQDLKKLTCQVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MTRTYENFOYLENKVKVQGFKNGP------LPLOSLLQRLRSGPCHLLLSLGLG
                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=BAB-14, and 129/SvJ;
MEDLINE=22151062; PubMed=12016228; DOI=10.1074/jbc.M203774200;
Tsuiji M., Fujimori M., Ohashi Y., Higashi N., Onami T.M.,
Hedrick S.M., Irimura T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50.1%; Score 870; DB 2; Length 332; 52.8%; Pred. No. 2.2e-64; ive 42; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   332 AA; 38067 MW; 76167D0D55E253E2 CRC64;
                                                                                                                                                                                                                                           01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Macrophage galactose-type C-type lectin 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P07306; 1DV8.
MGD; MG1:2385729; Mgl2.
GO; GO:0030246; F:carbohydrate binding; IDA.
                                                                                                                                                                                332 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00615; C TYPE LECTIN 1; 1. PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                           Q8JZN1 PRELIMINARY; PRT;
Q8JZN1;
01-OCT-2002 (TrEMBLrel. 22, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Biol. Chem. 277:28892-28901(2002)
EMBL; AX103461; AAM52097.1; -.
EMBL; AX103462; AAM52098.1; -.
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InterPro; IPR001304; Lectin C.
InterPro; IPR009640; lectin N.
InterPro; IPR009053; Prefoldin.
Pfam; PP00059; Lectin C; 1.
PRINTS; PR00354; Lectin N; I.
PRINTS; SMO0034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 52.8
Matches 171; Conservative
                         302 WVCEAGLGQTS 312
                                                                273 WVĆETEĽGKAN 283
                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                              Name=Mgl2,
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                                                                                                                                  RESULT 8
                                                                                                                                                       Q8JZN1
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                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 NSKFQRDLVTLRTDFSNFTSNTVAEIQALTSQGSSLEETIASLKAEVEGFKQERQAGVSE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOEHTTOKAHLGHCPHCPSVCVPVHSEMLLRVQQLVQDLKKLTCQVATLANNASTEGTCC 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 LRED--------HSRLLLHVKQLVSDVRSLSCQMAALRGNGS-ERICC 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 PVNWVEHQDSCYWFSHSGMSWAEAEKYCQLKNAHLVVINSREEQNFVQKYLGSAYTWMGL 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDPEGAWKWVDGTDYATGFQNWKPGQPDDWQGHGLGGGGEDCAHFHPDGRWNDDVCQRPYH 301
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RGD; 2160; Asgr1.

InterPro; IPR001253; Antifreezell.

InterPro; IPR001304; Lectin_C.

InterPro; IPR005640; Lectin_N.

Pfam; PF00055; Lectin_N.

Pfam; PF00954; Lectin_N.

PROMITS; PR00035; ANTIFREEZEII.

SWART; SW00034; CLECT; 1.

PROSITE; PS06015; C_TYPE_LECTIN_1; 1.

PROSITE; PS06015; C_TYPE_LECTIN_1; 1.

PROSITE; PS06015; C_TYPE_LECTIN_2; 1.

Calcium; Endocytosis; Glycoprotein; Lectin; Phosphorylation; Receptor;
                                                                                                         -1- MISCELLANEOUS: Calcium is required for ligand binding.
-1- MISCELLANEOUS: Two types of rat hepatic lectin have been identified, RHL-1 and RHL-2/3, having a relative abundance of 4:1.
-1- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 TRIYENFQYLENKVKVQGFKNGPLPLQSLLQRLRSGPCHLLLSLGLGLLLLVIICVVGFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                    SUBUNIT: Interacts with LASS2 (By similarity).
SUBCELLULAR LOCATION: Type II membrane protein.
TISSUE SPECIFICITY: Expressed exclusively in hepatic parenchymal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Endocycor.

By similarity.
By similarity.
N-linked (GlCNAc. ..) (Potential).
N-linked (GlCNAc. ..) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal-anchor for type II membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C-type lectin.
Endocytosis signal (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q -> R (in Ref. 2).
3BA2631A5E28A993 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 Q
32718 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane
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NCBI_TaxID=10090;
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DISULPID
DISULPID
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    TRANSMEM
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                                           DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence and expression in liver, testis and epididymis.";
Gene 148:237-244(1994).
-!- FUNCTION: Mediates the endocytosis of plasma glycoproteins to
which the terminal stalic acid residue on their complex
carbohydrate moieties has been removed. The receptor recognizes
terminal galactose and N-acetylgalactosamine units. After ligand
binding to the receptor, the resulting complex is internalized and
transported to a sorting organelle, where receptor and ligand are
disassociated. The receptor then returns to the cell membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PSO0615; C_TYPE_LECTIN 1; 1.
PROSITE; PSSO041; C_TYPE_LECTIN 2; 1.
Calcium; Endocytosis; Glycoprotein; Lectin; Phosphorylation; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: Interacts with LASS2 (By similarity).
SUBCELLULAR LOCATION: Type II membrane protein.
TISSUE SPECIFICITY: Expressed exclusively in hepatic parenchymal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=BALB/C; TISSUE=Liver;
MEDLINE=95047431; Pubmed=7958950; DOI=10.1016/0378-1119(94)90694-7;
MODIVOE R.S., Huber B.E.;
"The major form of the murine asialoglycoprotein receptor: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93176818; PubMed=8439566; DOI=10.1016/0167-4781(93)90300-3; Takezawa R., Shinzawa K., Watanabe Y., Akaike T.; "Determination of mouse major asialoglycoprotein receptor cDNA
                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                         LECH MOUSE STANDARD; PRT; 283 AA.
P34927; Q64363;
O1-FEB-1994 (Rel. 28, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Asialoglycoprotein receptor 1 (Hepatic lectin 1) (MHL-1) (ASGP-R)
(ASGPR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MISCELLANEOUS: Calcium is required for ligand binding. SIMILARITY: Contains 1 C-type lectin family domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochim. Biophys. Acta 1172:220-222(1993).
  297 GRWNDDVCQRHYHWICETELGKAS 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:88081; Asgrl.
InterPro; IPR001333; AntifreezeII.
InterPro; IPR001304; Lectin_C.
InterPro; IPR005640; lectin_N.
Pfam; PF00059; Lectin_C; 1.
PRINTS; PR00354; Lectin_N; 1.
PRINTS; PR0034; CLECT; 1.
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INIT_MET 0 0
DOMAIN 1 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, D13517; BAA02734.1; -. EMBL, U09362; AAB60441.1; -. EMBL; U08372; AAB60440.1; -. HSSP; P07306; 1DV8.
                                                                                                                                                                                                                                                                                Name=Asgrl; Synonyms=Asgr-1;
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence.";
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                                                                                           LECH MOUSE
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REDLINE=22388257; PubMod=1247932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Rlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,
A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarane P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Marxy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 LOEHTTOKAHLGHCPHCPSVCVPVHSEMLLRVQQLVQDLKKLTCQVATLNNNASTEGTCC 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 NSKFQRDLVTLRTDFSNFTSNTVAEIQALTSQGSSLEETIASLKAEVEGFKQERQAGVSE 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                        28; Gaps
                                                                       C-type lectin.

Endocytosis signal (Potential).

By similarity.

By similarity.

By similarity.

N-linked (GloNAc...) (Potential).

N-linked (GloNAc...) (Potential).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Signal-anchor for type II membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Macrophage galactose N-acetyl-galactosamine specific lectin 1.
                                                                                                                                                                                                                                                                                                                                                                               Length 283;
                                                                                                                                                                                                                                                                                                                                                                                                                                     71; Indels
                      protein (Potential).
Extracellular (Potential).
                                                                                                                                                                                                                                                                                                     -> T (in Ref. 1).
982A5D305AAE0D8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                               49.8%; Score 866; DB 1; 50.8%; Pred. No. 3.8e-64; rative 54; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 304 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=FVB/N; TISSUE=Mammary tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                          163 BY
275 BY
267 BY
74 N-
77 N-
145 N-
145 N-
150 I
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 50.8³
Matches 158; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WVCEAGLGQTS 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
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150 1
283 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=89197865; PubMed=3241002;

MEDLINE=89197865; PubMed=3241002;

Oda S., Sato M., Toyoshima S., Osawa T.;

Oda S., Sato M., Toyoshima S., Osawa T.;

Oda S., Sato M., Toyoshima S., Osawa T.;

for galactoses/N-acetyl-galactosamine from tumoricidal macrophages.";

J. Biochem. 104:600-605(1988).

-! FUNCTION: Recognizes terminal galactose and N-acetylgalactosamine macrophages and tumor cells.

-! SUBGINIT: Homooligomer.

-! SUBGINIT: Homooligomer.

-! SUBCELIULAR LOCATION: Type II membrane protein.

-! TISSUE SPECIFICITY: Expressed on the surface of activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 YENLONSRIEEKTQ--EPGKAPSQSFLWRILSWTHLLLFSLGLSLLLLVVVSVIGSQNSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 VSELQEHTTQKAHLGHCPHCPSVCVPVHSEMLLRVQQLVQDLKKLTCQVATLNNNASTEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 YENFOYLENKVKVQGFKNGPLPLQSLLQRLRSGPCHLLLSLGLGLLLLVIICVVGFQNSK
   Sato M., Kawakamyi K., Osawa T., Toyoshima S.;
"Molecular cloning and expression of cDNA encoding a galactose/N-
acetylgalactosamine-specific lectin on mouse tumoricidal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298 C-type lectin.
184 By similarity.
296 By similarity.
288 By similarity.
74 N-linked (GlCNAC. .) (Potential)
166 N-linked (GlCNAC. .) (Potential)
34596 MM, 3F79CD12C34F5BCC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal-anchor for type II membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR, JX0209; JX0209.

HSSP: P07306; 1DV8.

MGD; MGI: 96975; Mg1.

InterPro; IPR001304; Lectin C.

InterPro; IPR00131; Prefoldin.

InterPro; IPR00591; Prefoldin.

Pfam; PF003954; Lectin N; 1.

Pfam; PR00394; Lectin N; 1.

Pfam; PR00394; Lectin N; 1.

Pfam; PR00154; CLECTIN N; 1.

Pfam; PR00154; CLECTIN N; 1.

PROSITE; PS00015; CTYPE_LECTIN 1; 1.

PROSITE; PS00015; CTYPE_LECTIN 1; 1.

PROSITE; PS00015; CTYPE_LECTIN 2; 1.

PROSITE; PS00015; CTYPE_LECTIN 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 304;
                                                                                                                                                                                                                                                                                                                                                   SIMILĀRITY: Contains 1 C-type lectin family domain.
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Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytoplasmic (Potential)
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51.3%; Pred. No. 6.4e-59;
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                                                                                                         SEQUENCE OF 102-120 AND 137-151.
                                                                       J. Biochem. 111:331-336(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal-anchor; Transmembrane.
DOMAIN 1 35 (
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298
184
296
288
74
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304 AA;
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                                                                                                                                                                                                                                                                                                                                      macrophages.
                                                                                                                           STRAIN=C3H/HeN
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DISULFID
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FORDLVTLRTDFSNFTSNTVAELQALTSQGSSLEETIASLKAEVEGFKQERQAGVSELQE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 HTTQKAHLGHCPHCPSVCVPVHSEMLLRVQQLVQDLKKLTCQVATLNNNASTEGTCCPVN 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245 EGAWKWYDGTDYATGFQNWKPGQPDDWQGHGLGGGEDCAHFHPDGRWNDDVCQRPYHWVC 304
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Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalaka U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 YENLQNSRIEEKTQ--EPGKAPSQSFLWRILSWTHLLLFSLGLSLLLLVVVSVIGSQNSQ
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01-FEB-1996 (Rel. 33, Last sequence update)
05-UTL-2004 (Rel. 44, Least annotation update)
Macrophage asialoglycoprotein-binding protein 1 (M-ASGP-BP)
(Macrophage galactose/M-acetylgalactosamine-specific lectin) (MMGL).
Mame=Mgl1; Synonyms=Mgl;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 46.3%; Score 805; DB 2; Length 304; Best Local Similarity 51.6%; Pred. No. 5.3e-59; Matches 159; Conservative 43; Mismatches 100; Indels
                                                                                                                                                                            Strausberg R.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL: BC014B11; AAH14811.1; -. HSSP; P07306; 1DV8.
                                                                                                                                                                                                                                                                                                                                                                                                                     304 AA; 34622 MW; 2272E1ADA2C0262A CRC64;
                                                                                       and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  304 AA
                                                                                                                                                                                                                                         MGD; MGI:96975, MGII.
MGD; MGI:96975, MGII.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005529; F:sugar binding; IEA.
Pfam; PF000559; Lectin_C; 1.
Pfam; PF03954; Lectin_N; 1.
PRINTS; SM00515; CLECT; I.
PROSITE; PS00615; C_TYPE_LECTIN_I; 1.
PROSITE; PS50041; C_TYPE_LECTIN_Z; 1.
                                                                                                                          [2]
SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Mammary tumor;
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STRAIN=C3H/HeN;
MEDLINE=92268032; PubMed=1587794;
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P49300;
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                                                                    MGLSDPEGAWKWVDGTDYATGFQNWKPGQPDDWQGHGLGGGGDCAHFHPDGRWNDDVCQR 298
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SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUB=Mammary gland;

STRAIN=C57BL/6J; TISSUB=Mammary gland;

MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

A Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

A Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

A Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

A Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Matahiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawii J.,

A Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-format

T sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECUENCE FROM N.A.
STRAIN-CS7BL/6J; TISSUE-Mammary gland;
The FANTOM Consortium.
The FANTOM Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cons.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRANT=C57BL/6J; TISSUE=Mammary gland;
MEDLINE=20499374; PubMed=1042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Normalization and subtraction of cap-trapper-selected cDNAs-to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                   TCCPVNWVEHQDSCYWFSHSGMSWAEAEKYCQLKNAHLVVINSREEQNFVQKYLGSAYTW
                            ACCPLHWTEHEGSCYWFSESEKSWPEADKYCRLENSHLVVVNSLEEQNFLQNRLANVVSW
                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CS7BL/6J; TISSUE=Mammary gland; MEDLINE=99279273; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                         01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
MAR musculus 10 days lactation, adult female mammary gland cDNA, full-length enriched library, clone:D730047H02 product:similar to MACROPHAGE GALACTOSE N-ACETYL-GALACTOSAMINE SPECIFIC LECTIN.
MAR musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CS7BL/6J; TISSUE=Mammary gland;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM Consortium;
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                                                                                                                            PYHWVCEAGLGQTS 312
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291 TFRWICEMKLAKES 304
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                                                                                                                                                                                                                                PRELIMINARY;
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STRAIN=CS7BL/6J; TISSUE=Mammary gland;
A Adachi J. Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,
A Adachi J., Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,
A rakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
A Hanagaki T., Hara A., Hayatsu N., Hiramcto K., Hiracka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Koya S., Kurihara C.,
A Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
A Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
A Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
A Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
R EMBL, AkOB5751; BAC39530.1;
R HSSP, P07306; 1DV8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 IPSQSFLWRILSWTHLLLFSLGLSLLLVVISVIGSQNSQLRRDLGTLRAILDNTTSKIK 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 LPLQSLLQRLRSGPCHLLLSLGLGLLLLVIICVVGFQNSKFQRDLVTLRTDFSNFTSNTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145 VHSEMLLRVQQLVQDLKKLTCQVATLNNNASTEGTCCPVNWVEHQDSCYWFSHSGMSWAE
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[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 AA; 41010 MW; AAACBB748C66A231 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45.5%; Score 791; DB 2; Lv 47.0%; Pred. No. 9.8e-58; tive 40; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  277 GGGEDCAHFHPDGRWNDDVCQRPYHWVCEAGLGQTS 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        314 GGGEDCAHFSYDGRWNDDVCQRHYYWICETELGKAS 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        306 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0016020; C:membrane; IEA.
GO; GO:0005529; F:sugar binding; IEA.
InterPro; IPR001304; Lectin_C.
InterPro; IPR005640; lectin_N.
InterPro; IPR009053; Prefoldin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam, PF00059; Lectin_C; 1. Pfam; PF03954; Lectin_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 47.0%
Matches 158; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HBxAg-binding protein.
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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  139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99 SSSTLTEVQAISTHGGSVGDKITSLGAKLEKQQQDLKA-----DHDALLFHLKHFP--- 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200 MSWAEAEKYCOLKNAHLVVINSREEQNFVQKYLGSAYTWMGLSDPEGAWKWVDGTDYATG 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                  39 FLKGPPPAQPLAQRLCSMVCFSLLALSFNILLLVVICVTGSQSAQLQAELRSLKEAFSNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 TSNTVAEIQALTSQGSSLEETIASLKAEVEGFKQERQAGVSELQEHTTQKAHLGHCPHCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 SVCVPVHSEMLLRVQQLVQDLKKLTCQVATLANNASTEGTCCPVNWVEHQDSCYWFSHSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=86016723; PubMed=3863106;
Spiess M., Lodish H.F.;
"Sequence of a second human asialoglycoprotein receptor: conservation of two receptor genes during evolution.";
Proc. Natl. Acad. Sci. U.S.A. 82:6465-6469(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the
                                                                                                                                                                                                                                                                                                                                                                                                                          20 FKNGPLPLQSLLQRLRSGPCHLLLSLGLGLLLLVIICVVGFQNSKFQRDLVTLRTDFSNF
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 YKNWAVTQPDNWHGHELGGSEDCVEVQPDGRWNDDFCLQVYRWVCEKRNATGE 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260 FQNWKPGQPDDWQGHGLGGGEDCAHFHPDGRWNDDVCQRPYHWVCEAGLGQTSQ 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LECI HUMAN STANDARD; ...., P013167; 000448; Q03969; 01-APR-1988 (Rel. 07, Created) 01-APR-1988 (Rel. 07, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update) Asialoglycoprotein receptor 2 (Hepatic lectin H2) (ASGP-R) (ASGPR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Paietta E., Stockert R.J., Racevskis J.; "Differences in the abundance of variably spliced transcripts for second asialoglycoprotein receptor polypeptide, H2, in normal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                  28;
                                                                                                                                                                                                                                                                                                                                         Length 306;
                                                                                                                                                                                                                                                                                                                                                                                  79; Indels
                   Lu Y., Liu Y., Cheng J.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF529374; AAQ09608.1; -.
                                                                                                GO, GO:0016020; C:membrane; IEA.
GO; GO:0005529; F:sugar binding; IEA.
InterPro; IPR001304; Lectin_C.
InterPro; IPR00560; lectin_N.
Pfam; PF03954; Lectin_N; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00015; C_TYPE_LECTIN 1; 1.
PROSITE; PS00015; C_TYPE_LECTIN 2; 1.
SEQUENCE 306 AA; 34655 MW; F53B06C41AE80D03 CRC64;
                                                                                                                                                                                                                                                                                                                                       44.1%; Score 767; DB 2;
48.6%; Pred. No. 8.1e-56;
                                                                                                                                                                                                                                                                                                                                                                                44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=92184202; PubMed=1371982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 3).
TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatology 15:395-402(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rransformed human liver.";
                                                                                                                                                                                                                                                                                                                                                                                  Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                   P07306; 1DV8.
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Nausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A phykins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., Wiskin T.B., Toshiyuki S., Carninci P., Frange C.,
Raba S.S., McEwan P.J., McKernan R.J., Mahre J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Wilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rabey J., Helton B., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schmerch A., Schein J.B., Jones S.J.M., Marra M.A.;
T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its meeb by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MIM; 108361; -.
GO; GO:0004813; F:asialoglycoprotein receptor activity; TAS.
GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                terminal galactose and N-acetylgalactosamine units. After ligand binding to the receptor, the resulting complex is internalized and transported to a sorting organelle, where receptor and ligand are disassociated. The receptor then returns to the cell membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gurface.
Subsurf: The functioning ligand-binding unit of this receptor is
thought to be at least a dimer. Interacts with LASS2.
SUBCELLULAR LOCATION: Type II membrane protein.
ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=P07307-3; Sequence=VSP_003060, VSP_003061;
TISSUE SPECIFICITY: Expressed exclusively in hepatic parenchymal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- FUNCTION: Mediates the endocytosis of plasma glycoproteins to which the terminal sialic acid residue on their complex carbohydrate moieties has been removed. The receptor recognizes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=11543633; DOC=10.1006/geno.2001.6614; Pan H., Qin W.-X., Huo K.-K., Wan D.-F., Yu Y., Xu Z.-G., Hu Q.-D., Gu K.T., Zhou X.-M., Jiang H.-Q., Zhang P.-P., Huang Y., Li Y.-Y., Gu J.-R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cloning, mapping, and characterization of a human homologue of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cells.
MISCELLANEOUS: Calcium is required for ligand binding.
SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=P07307-2; Sequence=VSP_003060;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=P07307-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             yeast longevity assurance gene LAG1.";
Genomics 77:58-64(2001).
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EMBL; U97197; AAB58308.1; -.
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PIR; A25179; LNHU2A.
HSSP; P07306; 1DV8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERACTION WITH LASS2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HGNC:743; ASGR2.
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AFSNFSSSTLTEVOALSTHGGSVGDKITSLGAKLEKQQODLKA-----DHDALLFHLKH 152
                                                                                                                                                                                                                                                                                                                                                                                                 75 DFSNFTSNTVAEIQALTSQGSSLEETIASLKAEVEGFKQERQAGVSELQEHTTQKAHLGH 134
                                                                                                                                                                                                                                                                                                                                                                                                                                         CPHCPSVCVPVHSEMLLRVQQLVQDLKKLTCQVATLNNNASTEGTCCPVNWVEHQDSCYW 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                              153 FP-------VDLRFVACQMELLHSNGS-QRTCCPVNWVEHQGSCYW 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FSHSGKAWAEAEKYCQLENAHLVVINSWEEQKFIVQHTNPFNTWIGLTDSDGSWKWVDGT 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FSHSGMSWAEAEKYCQLKNAHLVVINSREEQNFVQKYLGSAYTWMGLSDPEGAWKWVDGT 254
                                                                                                                                                                                                                                                                                                                                                                  39 FLKGPPPAQPLAQRLCSMVCFSLLALSFNILLLVVICVTGSQSEGHRGAQLQAELRSLKE 98
                                                                                                                                                                                                                                                                                                                                                       20 FKNGPLPLQSLLQRLRSGPCHLLLSLGLGLLLLVIICVVGFQN----SKFQRDLVTLRT 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DYATGFQNWKPGQPDDWQGHGLGGGEDCAHFHPDGRWNDDVCQRPYHWVCEAGLGQTSQ 313
                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=CSPBL/6; TISSUE=Liver;
MEDIJNE=91027942; PubMed=2223888; DOI=10.1016/0167-4781(90)90216-0;
Sanford J.P., Doyle D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Asialoglycoprotein receptor 2 (Hepatic lectin 2) (MHL-2) (ASGP-R)
(ASGPR).
                                                                                                                                                                                                                                                                                                                                79; Indels 33;
                                                                                                                                                                                                                                                                                                              DB 1; Length 311;
                                                                                                                                                                                                                                                                              /FTId=VSP_003061.
82C78FECBFEBA316 CRC64;
                                                                                                                                                                                                                                                Alberns
Frid=VSP 00306u.
Missing (in isoform 3).
                                                                                                                                                                                                                                                                                                            Score 754.5; DB 1
Pred. No. 9.2e-55;
                                                                                                                                                                                                                                                                                                                                  44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 AA
                                                                                                                                                                                                                                                                                        311 AA; 35191 MW;
                                                                                                                                                                                                                                                                                                              43.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Asgr2; Synonyms=Asgr-2;
                                                                                                                                                                                                                                                                                                                                   143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LECI MOUSE
P24721;
                                                                                                                                                                                                                                                                                                                                                                                                                                          135
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                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                              Query Match
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LECI_MOUSE
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SEQUENCE FROM N.A.

STRAIN=FVRIAN ; IISSUS=Liver;

STRAIN=FVRIAN; IISSUS=Liver;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Attaubberg R.D., Felingold E.A., Grouse L.H., Derge J.G.,

Attauberg R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Attachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Boatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., McKernan R.J., Malek J.A., Gunazatne P.H.,

Raba S.S., Loquellano N.A., Sodergren E.J., Lu X., Gibbs R.A.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Brown A., Schnerch A., Schmit J. Jones B.J., Marra M.A.,

R. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: Mediates the endocytosis of plasma glycoproteins to which the terminal sialic acid residue on their complex carbohydrate moieties has been removed. The receptor recognizes terminal galactose and N-acetylgalactosamine units. After ligand binding to the receptor, the resulting complex is internalized and transported to a sorting organalle, where receptor and ligand are disassociated. The receptor then returns to the cell membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO0356; ANTIFREZZII.
PROSITE; PSO0615; C_TYPE_LECTIN_1; 1.
PROSITE; PSSO041; C_TYPE_LECTIN_2; 1.
Calcium; Endocytosis; Glycoprotein; Phosphorylation; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- SUBUNIT: Interacts with LASS2 (By similarity).
-1- SUBCELLULAR LOCATION: Type II membrane protein.
-1- TISSUE SPECIFICITY: Expressed exclusively in hepatic parenchymal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal-anchor for type II membrane protein (Potential).
Extracellular (Potential).
C-type lectin.
By similarity.
By similarity.
By similarity.
  of
"Mouse asialoglycoprotein receptor cDNA sequence: conservation receptor genes during mammalian evolution."; Biochim. Biophys. Acta 1087:259-261 (1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- MISCELLANEOUS: Calcium is required for ligand binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X53042; CAA37211.1; --
EMBL; BC011197; AAH11197.1; --
EMBL; S01165; S13165.
HSSP; P07306; 1DV8.
MGD; MGI.88082; ABGY2.
INTERPRO; IPR002353; AntifreezeII.
INTERPRO; IPR002354; Lectin_C.
InterPro; IPR005640; Lectin_N.
PÉam; PF00059; Lectin_N.
PÉam; PF00059; Lectin_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences."
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295
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293
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DOMAIN 1
TRANSMEM 59
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84 VAEIQALTSQGSSLEETIASLKAEVEGFKQERQAGVSELQEHTTQKAHLGHCPHCPSVCV 143
                                                                                                                                                                                103 LMEFGALDTLGGSTNAILTSWLAQLEEKQQQLKA-----DHSTLLFHLKHFP----- 149
                                                                                                                                                                                                                    144 PVHSEMLLRVQQLVQDLKKLTCQVATLNNNASTEGTCCPVNWVEHQDSCYWFSHSGMSWA 203
                                                                                                                                                                                                                                   204 EAEKYCOLKNAHLVVINSREEQNFVOKYLGSAYTWMGLSDPEGAWKWVDGTDYATGFQNW 263
                                                                                                                                                                                                                                                                                     Query Match 38.6%; Score 671.5; DB 1; Length 301;
Best Local Similarity 46.1%; Pred. No. 7.8e-48;
Matches 130; Conservative 42; Mismatches 75; Indels 35; Gaps
97 97 N-linked (GlCNAC. ..) (Potential).
165 165 N-linked (GlCNAC. ..) (Potential).
298 N-linked (GlCNAC. ..) (Potential).
301 AA, 34907 MW, 3A29FlAFBA68F298 CRC64;
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CARBOHYD
CARBOHYD
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Search completed: May 27, 2005, 12:48:52 Job time : 68 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Run on:

May 27, 2005, 12:44:45 ; Search time 17 Seconds (without alignments) 1788.500 Million cell updates/sec

US-10-829-107-4 1738 1 MTRTYENPQYLENKVKVQGF......QRPYHWVCEAGLGQTSQESH 316 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hepatic lectin H1	lectin M-ASGP-BP p	hepatic lectin - r	asialoglycoprotein	lectin, galactose/	asialoglycoprotein	asialoglycoprotein	hepatic lectin 2 -	Kupffer cell recep	HIV gp120-binding	scavenger receptor	IgE Fc receptor II	IgB Fc receptor, 1	ij	IGE Fc receptor II	perlucin - Halioti	type II lectin-lik	versican precursor	proteoglycan core	aggrecan - bovine	versican precursor	chondroitin sulfat	versican precursor	neurocan - mouse	versican precursor	aggrecan precursor	proteoglycan core	aggrecan precursor	aggrecan precursor
SUMMARIES	01	LINHUI	A42230	LNRTL	S29855	JX0209	LNHU2A	S13165	LNRT2	A28166	A46274	JC7595	S34198	LNMSER	LNCHL	LNHUER	S78774	. JC7608	A55535	A39808	T42630	A60979	A47171	T14274	S52781	T42389	I50421	A28452	A55182	A39086
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	Length	291	306	284	284	304	311	301	301	550	404	742	309	331	207	321	155	237	2397	1340	2327	2409	3562	1643	1268	3381	2109	2124	13	2415
de	Query Match	53.1	51.0	50.6	50.5	46.3	43.4	38.6	37.7	18.8	18.2	18.0	16.6	16.5	16.2	15.8	14.9	14.6	14.0	13.8	13.8	٠	13.8	13.8	13.7	13.7		13.3		13.1
	Score	923.5	887	879	877	804	754.5	671.5	655.5	326.5	316	313	288.5	287	281	274.5	259	253	243.5	240	240	239.5	239.5	239	238.5	237.5	236.5	232	228	228
	Result No.	п	8	e	4	S	9	7	80	6	10	11	12	13	.14	15	16	17	18	19	20		22			25	26	27	28	29

neurocan precursor	brevican precursor	brevican - human (	brevican precursor	brevican precursor	lectin BRA3-1 prec	echinoidin - sea u	lectin BRA3-2 prec	endothelial leukoc	gene 17.5 protein	lymphocyte early a	lectin - Iberian r	antifreeze protein	L-selectin precurs	hypothetical prote	E-selectin precurs
S28764	A54423	T46256	S57653	S49126	LNRC1	A26697	LNRC3	I46709	150146	JH0822	S32489	A34313	JC5377	T34115	B42755
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257	912	330	883	883	162	147	162	551	257	199	172	163	372	262	612
12															
_	12.9	12.8	12.6	12.6	11.7	11.4	11.3	10.8	10.8	10.7	10.6	10.4	10.4	10.3	10.2
13.0	223.5 12.9				204 11.7		196 11.3					181 10.4			178 10.2

## ALIGNMENTS

RESULT 1  INHU1  hepatic lectin H1 - human  hepatic lectin H1 - human  N.Alternate names: asialoglycoprotein receptor H1 (ASGP-H1)  C,Species: Homo sapiens (man)  C,Species: Homo sapiens (man)  C,Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004  C,Accession A22509  R,Spiess, M.; Schwartz, A.L.; Lodish, H.F.  J. Biol. Chem. 260, 1979-1982, 1985  A,Ritle: Sequence of human asialoglycoprotein receptor cDNA: an internal signal sequence A,Reference number: A22509; MUID:85130911; PMID:2982798
A; Molecule type: mRNA A; Residues: 1-29168D1> A; Residues: 1-29168D1> A; Residues: 1-29168D1> C; Comment: This receptor is expressed in mammals exclusively in hepatic parenchymal cells C; Comment: This receptor is expressed in mammals exclusively in hepatic parenchymal cells C; Comment: By homology with the R1 receptor, the initiator Met is removed after translat C; Comment: A cytoplasmic serine residue is phosphorylated. C; Genetics:
A;Gene: GDB:ABGRI A;Croser-references: GDB:118754; OMIM:108360 A;Map position: 17p13-17p1 C;Superfamily: hepatic lectin; C-type lectin homology C;Keywords: endocytosis; glycoprotein; lectin; phosphoprotein; receptor; transmembrane pi F;2-291/Product: hepatic lectin H1 #status predicted <mat> F;2-240/Domain: intracellular #status predicted <mnt> F;4-159/Domain: transmembrane #status predicted <mna> F;6-291/Domain: extracellular #status predicted <ext></ext></mna></mnt></mat>
F:154-277/Domain: C-type lectin homology <lch> F:79,147/Binding site: carbohydrate (Asn) (covalent) #status predicted</lch>

29; Gaps DB 1; Length 291; Indels Query Match 53.1%; Score 923.5; DB 1; Best Local Similarity 54.6%; Pred. No. 1.5e-67; Matches 172; Conservative 47; Mismatches 67;

1 MIRIYENFQYLENKVK-VQGFKNGPLPLQSLLQRLRSGPCHLLLSLGLGLLLLVIICVVG

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5

29

120 SELOEHTTOKAHLGHCPHCPSVCVPVHSEMILRVQQLVQDLKKLTCQVATLANNNASTEGT 179 60 FONSKFORDLVTLRTDFSNFTSNTVAELQALTSQGSSLEETIASLKAEVEGFKQERQAGV 119 a ò g ò g

180 CCPVNWVEHQDSCYWFSHSGMSWAEAEKYCQLKNAHLVVINSREEQNFVQKYLGSAYTWM 239 153 CCPVNWVEHERSCYWFSRSGRAWADADNYCRLEDAHLVVVTSWEEQKFVQHHIGPVNTWM 212 g ò

240 GLSDPEGAWKWVDGTDYATGFQNWKPGQPDDWQGHGLGGGEDCAHFHPDGRWNDDVCQRP 299

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Tue May

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A; Molecule type: mRNA
A; Residues: 1-60, K', 62-210 < HOL>
A; Experimental source: clone 22; clone 1
A; Accession: B94020
A; Molecule type: mRNA
A; Residues: 92-284 < HO2>
A; Molecule type: mRNA
A; Residues: 92-284 < HO2>
B; Molecule type: mRNA
A; Note: clone 22 codes for a terminator at residue 210
B; Watts, C.
Bioaci, Rep. 6, 527-534, 1986
A; Fitle: Isolation and expression of cDNA clones for a rat liver asialoglycoprotein recental complex: A54727; MUID: 87026895; PMID: 2945599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A54727
A; Molecule type: mRNA
A; Experimental source: liver
C; Comment: Two types of rat hepatic lectin have been identified, RHL-1 and RHL-2/3, havi
C; Comment: Two types of rat hepatic lectin have been identified, RHL-1 and RHL-2/3, havi
C; Comment: The unusual orientation of this protein across the membrane is postulated to
A; Introns: 23/1; 62/1; 94/1; 118/1; 197/3; 233/2
C; Genetics:
A; Introns: 23/1; 62/1; 94/1; 118/1; 197/3; 233/2
C; Superfamily: hepatic lectin; Retatus predicted chAT>
F; 2.294/Product: hepatic lectin #status predicted chAT>
F; 2.39/Domain: intracellular #status predicted chAT>
F; 2.39/Domain: extracellular #status predicted chAM>
F; 2.30/Domain: extracellular #status predicted chAM>
F; 2.30/Domain: extracellular #status predicted chAM>
F; 2.30/Domain: contacellular #status predicted chAM>
F; 2.30/Domain: contacellula
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C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: 829855
R;Takcaawa, R.; Shinzawa, K.; Watanabe, Y.; Akaike, T.
Biochim. Biophys. Acta 1172, 220-222, 1993
A;Title: Determination of mouse major asialoglycoprotein receptor cDNA sequence.
A;Reference number: 829855; MUID:93176818; PMID:8439566
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 QNSKFQRDLVTLRTDFSNFTSNTVAEIQALTSQGSSLEETIASLKAEVEGFKQERQAGVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 DLRED------HSRLLLHVKQLVSDVRSLSCQMAALRGNGS-ERIC 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        153 CPINWVEYEGSCYWFSSSVKPWTEADKYCQLENAHLVVVTSWEEQRFVQQHMGPLNTWIG 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MTRIYENFOYLENKVKVQGFKNGPLPLQSLLQRLRSGPCHLLLSLGLGLLLLVIICVVGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CPVNWVBHQDSCYWFSHSGMSWAEAEKYCQLKNAHLVVINSREEQNFVQKYLGSAYTWMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;153-276/Domain: C-type lectin homology <LCH>
F;75,78,146/Binding site: carbohydrate (Agn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.6%; Score 879; DB 1; Length 28 51.3%; Pred. No. 6.1e-64; tive 52; Mismatches 72; Indels
              A; Reference number: A94020; MUID:85063786; PMID:6095287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 HWVCEAGLGQTS 312
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Ba-Peb-1986 #sequence revision 04-Dec-1986 #text_change 09-Jul-2004
C;Accession: A92497; A94020; A54377; A03166
R;Leung, J.O.; Holland, E.C.; Drickamer, K.
J. Biol. Chem. 260, 12523-12527, 1985
A;Title: Characterization of the gene encoding the major rat liver asialoglycoprotein re
A;Reference number: A92497; MUID:86008335; PMID:2995379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Species: Rattus noveegicus (Norway rat)
C; Species: Rattus noveegicus (Norway rat)
C; Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 09-Jul-2004
C; Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 09-Jul-2004
C; Date: 19-Jun-1992 #sequence_revision 1:; Kawasaki, T.
J. Biol. Chem. 265, 11295-11298, 1990
J. Sequence analysis of CDNA encoding the macrophage lectin A; Reference number: A42230; MUD: 90293078; PMID: 2358462
A; Accession: A42230
A; A
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C;Superfamily: hepatic lectin; C-type lectin homology
F;175-298/Domain: C-type lectin homology <LCH>
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*Holland, B.C.; Leung, J.O.; Drickamer, K.
Proc. Natl. Acad. Sci. U.S.A. 81, 7338-7342, 1984
A;Title: Rat liver asialoglycoprotein receptor lacks a cleavable NH-2-terminal signal se
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213 GLHDQNGPWKWVDGTDYETGFKNWRPEQPDDWYGHGLGGGEDCAHFTDDGRWNDDVCQRP 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 QNSQLRRDLETLRTTLDNTTSNTKAELQALASRGDSLQTGINSLKVEVDDHGQELQAGRG 118
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                                                                                                                                               300 YHWVCEAGLGQTSQE 314
                                                                                                                                                                                                                                          273 YRWVCETELDKASOE 287
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Best Local Similarity 54.8%;
Matches 177; Conservative
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A; Residues: 1-284 <LEU>
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RiPaietta, E.; Stockert, R.J.; Racevakia, J.
Hepatology 15, 395-402, 1992
Aritle: Differences in the abundance of variably spliced transcripts for the second asia
A,Reference number: 137995; WIID:92184202; PMID:1371982
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A;Molecule type: mRNA
A;Cross-references: EMBL:X55283; NID:g34354; PIDN:CAA38997.1; PID:g34355
B;Yuk, M.H.; Lodish H.F.;Typy
A;Coll Biol. 123, 1735-1749, 1993
A;Title: Two pathways for the degradation of the HZ subunit of the asialoglycoprotein recaptoring to the number: A49466; MUID:94103329; PMID:8276894
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A;Molecule type: protein
A;Residues: 87-98 <YU2>
C;Comment: The functioning ligand-binding unit of this receptor is thought to be at least
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R;Lederkremer, G.Z.; Lodish, H.F.
J. Biol. Chem. 266, 1237-1244, 1991
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61 LRRDLGTLRATLDNTTSKIKAEFQSLDSRADSFEKGISSLKVDVEDHRQELQAGRDLSQK 120
                                                                                                                                    121 VTSL-ESTVEKRE-----QALKTDLSDLTDHVQQLRKDLKALTCQLANLKNNGS-EV
                                                                                                                                                                                                                                 VSELQEHTTQKAHLGHCPHCPSVCVPVHSEMLLRVQQLVQDLKKLTCQVATLNNNASTEG
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C,Superfamily: hepatic lectin; C-type lectin homology
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A;Residues: 69-99 <LED>
A;Cross-references: GB:M38420; NID:g184395
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A;Residues: 69-81,87-99 <LE2>
A;Cross-references: GB:M38420; NID:9184395
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291 TFRWICEMKLAKES 304
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A; Residues: 1-311 <SPI>
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R;Oda, S.; Sato, M.; Toyoshima, S.; Osawa, T.
B;Oda, S.; Sato, M.; Toyoshima, S.; Osawa, T.
A;Title: Purification and characterization of a lectin-like molecule specific for galact A;Reference number: PX0009; MUID:89197865; PMID:3241002
A;Accession: PX0009
A;Molecule type: protein
A;Residues: 102-120;137, X', 139-151 < ODA>
C;Superfamily: hepatic lectin; C-type lectin homology
C;Superfamily: hepatic lectin; Macrophage; transmembrane protein
F;36-61/Domain: transmembrane Heatuue predicted <TRA>
F;74,166/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A,Reference number: JX0209, MUID:92268032, PMID:1587794
                                                                    A; Cross-references: UNIPROT: Q91Y84; EMBL:D13517; NID:g220480; PIDN:BAA02734.1; PID:g2204
C; Superfamily: hepatic lectin; C-type lectin homology
C; Keywords: glycoprotein; transmembrane protein
P;153-276/Domain: C-type lectin homology < LCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELQEHTTQKAHLGHCPHCPSVCVPVHSEMLLRVQQLVQDLKKLTCQVATLNNNASTEGTC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CPVNWVEHQDSCYWFSHSGMSWAEAEKYCQLKNAHLVVINSREEQNFVQKYLGSAYTWMG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSDPEGAWKWVDGTDYATGFQNWKPGQPDDWQGHGLGGGEDCAHFHPDGRWNDDVCQRPY 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QNSKFQRDLVTLRTDFSNFTSNTVAEIQALTSQGSSLEETIASLKAEVEGFKQERQAGVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JX0209
Jeffin, galactose/N-acetylgalactosamine-specific - mouse
Jectin, galactose/N-acetylgalactosamine-specific - mouse
Jectin, galactose/N-acetylgalactosamine
C.Species: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C.Species: 30-Jun-1992 #sequence_revision 30-Jul-1992 #text_change 09-Jul-2004
C.Species: 30-Jul-1992 #sequence_revision 30-Jul-1992 #text_change 09-Jul-2004
C.Species: 30-Jul-1992 #sequence_revision 30-Jul-1992 #text_change 09-Jul-2004
C.Species: 30-Jul-1992 #sequence_revision 30-Jul-1992 #text_change 09-Jul-1992
C.Species: 30-Jul-1992 #sequence_revision 30-Jul-1992 #text_change 09-Jul-1992 #text_change 09-Jul-1992 #text_change 09-Jul-1992 #text_change 09-Jul-1992 #text_change 09-Jul-1992 #text_change 09-Jul-1992 #text_change 09-Jul-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MTRIYENFQYLENKVKVQGFKNGPLPLQSLLQRLRSGPCHLLLSLGLGLLLLVIICVVGF
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                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                     28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46.3%; Score 804; DB 2; Length 304; 51.3%; Pred. No. 8.2e-58; Indels 1ive 40; Mismatches 95; Indels 1
                                                                                                                                                                                                                                                                         Length 284;
                                                                                                                                                                                                                                                                                                                                                 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.5%; Score 877; DB 2;
51.3%; Pred. No. 8.9e-64;
iive 54; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               larity 51.3%;
Conservative
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Best Local Similarity 51.3
Matches 160; Conservative
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A, Molecule type: mRNA
A, Residues: 1-304 <SAT>
                                        1-284 <TAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161;
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C;Superfamily: hepatic lectin; C-type lectin homology
C;Keywords: glycoprotein; liver; transmembrane protein
F;170-293/Domain: C-type lectin homology <LCH>
C; Keywords: alternative splicing; endocytosis, glycoprotein; lectin, liver; phosphoprote F;1-311/Product: asialoglycoprotein receptor H2a #status predicted <MAT1>F;1-81,87-311/Product: asialoglycoprotein receptor H2b #status predicted <MAT2>F;1-58/Domain: intracellular #status predicted <INT>F;1-58/Domain: intracellular #status predicted <INT>F;1-53,43-81,87-311/Product: asialoglycoprotein receptor H2c #status predicted <MAT3>F;1-59-78/Domain: transmembrane #status predicted <IYM>F;79-311/Domain: extracellular #status predicted <EXT>F;79-311/Domain: C-type lectin homology <LGH+F;177-300/Domain: C-type lectin homology <LGH+F;102,170,305/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: S13165
R; Sanford, J.P.; Doyle, D.
Biochim Biophys. Acta 1087, 259-261, 1990
A; Title: Mouse asialoglycoprotein receptor CDNA sequence: conservation of receptor genes A; Reference number: S13165; MUD:91027942; PMID:2223888
A; Accession: S13165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      153 FP------VDLRFVACQMELLHSNGS-QRTCCPVNWVEHQGSCYW 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  195 PSHSGMSWAEAEKYCQLKNAHLVVINSREEQNFVQKYLGSAYTWMGLSDPEGAWKWVDGT 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 VAEIQALTSQGSSLEETIASLKAEVEGFKQERQAGVSELQEHTTQKAHLGHCPHCPSVCV 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       asialoglycoprotein receptor - mouse
N,Alternate names: hepatic lectin
C;Species: Mus musculus (house mouse)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: 313165
R;Sanford, J.P.; Dovle. D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39 FLKGPPPAQPLAQRLCSWVCFSLLALSFNILLLVVICVTGSQSEGHRGAQLQAELRSLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75 DFSNFTSNTVAEIQALTSQGSSLEETIASLKAEVEGFKQERQAGVSELQEHTTQKAHLGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PVHSEMILLRVQQLVQDLKKLTCQVATLNNNASTEGTCCPVNWVEHQDSCYWFSHSGMSWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 FKNGPLPLQSLLQRLRSGPCHLLLSLGLGLLLLVIICVVGFQN----SKFQRDLVTLRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204 EAEKYCOLKNAHLVVINSREEONFVOKYLGSAYTWMGLSDPEGAWKWVDGTDYATGFONW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33;
                                                                                                                                                                                                                                                                                                                                                                                                       Score 754.5; DB 1; Length 311;
Pred. No. 8.9e-54;
1; Mismatches 79; Indels 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 301;
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~hes 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
38.6*; Score 6/1.5; Best Local Similarity 46.1*; Pred. No. 4.8e
Matches 130; Conservative 42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   43.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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A; Residues: 1-301 <SAN>
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District lectin 2 - rat

Nighternate names: satisfoglycoprotein receptor RHL-2/3 (ASGP-R2/3)

Cipecies: Rattus norvegicus (Norvey rat)

RHalberg, D.F.; Wager, R.E.; Farral, D.C.; Hildreth IV, J.; Quesenberry, M.S.; Loeb, J. Biol. Chem. 262, 988-933, 1987

A; Rattie: Major and minor forms of the rat liver asialoglycoprotein receptor are independently Reference number: A28462; MUID:8750656; PMID:3597443

A; Reference number: A28462

A; Molecule type: maxA

A; Residues: 1-301 <AHL>
A; Accession: A28462

A; Molecule type: protein

A; Residues: Bel-66, Y, 120; 129-158; 177-182, Y, 184, Y, 186-189; 192-290, C', 292

R; Sanford, J.P.; Elliott, R.W.; Doyle, D.

By 7, 721-728, 1988

A; Molecule type: maxA

A; Reference number: A31601; MUID:89170119; PMID:3234178

A; Residues: 1-301 <SAN>
A; Reference number: A31601; MUID:89170119; PMID:3234178

A; Residues: 1-301 <SAN>
A; Reference number: A36888; MUID:872885; PMID:360647

A; Rickernce number: A26888; MUID:872885; PMID:360647

A; Recession number: A26888; MUID:872885; PMID:360647

A; Molecule type: RNA
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A; Residues: 1-152,'A',154-201,'I',203-259,'C',261-301 <MCP>
A; Residues: 1-152,'A',154-201,'I',203-259,'C',261-301 <MCP>
A; Residues: 1-152,'A',154-201,'I',203-259,'C',261-301 <MCP>
A; Residues: 1-152,'A',154-201,'I',203-259,'C',261-301. PIDD: 9206649
A; Note: the authors translated the codon GCA four residue 153 as Arg and ATT for residue;
B; Drickamer, K.; Mamon, J.F.; Binns, G.; Leung, J.O.
J. Biol. Chem. 259, 770-778, 1984
A; Title: Primary structure of the rat liver asialoglycoprotein receptor: structural evide
A; Reference number: A25417; MUD: 84111554; PMID: 6319386
A; Accession: A25417
A; Rejerence number: A25417; MUD: 84111554; PMID: 6319386
C; Comment: Calcium is required for ligand binding.
C; Comment: Calcium is required for ligand binding.
C; Superfamily: hepatic lectin, C-type lectin homology
C; Keywords: endocytosis; glycoprotein; lectin; liver; receptor; transmembrane #status predicted <INT>
F; 1-77/Domain: intracellular #status predicted <INT>
F; 78-301/Domain: extracellular #status predicted <INT>
F; 78-301/Domain: c-type lectin homology <INT>
F; 78-301/Domain: C-type lectin homology <INT>
F; 77-301/Domain: C-type lectin homology <INT</INT
F; 77-301/Domain: C-type lectin hom
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264 KPGQPDDWQGHGLGGGEDCAHFHPDGRWNDDVCQRPYHWVCE 305
                                                                                             253 AFTQPDNWQGHEQGGGEDCAEILSDGHWNDNFCQQVNRWVCE 294
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40.1%; Pred. No. 9.5e-46;
tive 55; Mismatches 90
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A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                      RESULT 9
A28166
Kupffer cell receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C;Accession: A38674, A28166
R;Hoyle, G.W.; Hill, R.L.
J; Biol. Chem. 266, 1850-1857, 1991
A;Reference number: A38674, MUID:91107689; PMID:1846367
A;Accession: A38674, MUID:9110769
A;Accession: A38674, MUID:9110769
A;Accession: A38674, MUID:910716, GB:M55532; NID:g203362; PIDN:AAA40892.1; PID:g203363
A;Cross-references: UNIPROT:P10716; GB:M55532; NID:g203362; PIDN:AAA40892.1; PID:g203363
A;Title: Molecular cloning and sequencing of a cDNA for a carbohydrate binding receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10

#46274
HIV 49120-binding C-type lectin - human
HIV 49120-binding C-type lectin - human
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
R;Curtis, B.M.; Scharnowske, S.; Wateon, A.J.
Proc. Natl. Acad. Sci. U.S.A. 89, 8356-8360, 1992
A;Title: Sequence and expression of a membrane-associated C-type lectin that exhibits CD
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                                                                                                         VSELQEHTTQKAHLGHCPHCPSVCVPVHSEMLLRVQQLVQDLKKLTCQVATLNNNASTEG 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236 YTWMGLSD--PEGAWKWVDGT--DYATGFQNWKPGQPDDWQGHGLGGGEDCAHFHPDGRW 291
  221
                                                                                     281
                      154 TLTCQLAFFLSNGT---ECCPVNWVEFGGSCYWFSRDGLTWAEADQYCQMENAHLLVINS
KLTCQVATLNNNASTEGTCCPVNWVEHQDSCYWFSHSGMSWAEAEKYCQLKNAHLVVINS
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                                                                                   REEQNFVQKYLGSAYTWMGLSDPEGAWKWVDGTDYATGFQNWKPGQPDDWQGHGLGGGED
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A,Molecule type: mRNA
A,Residues: 1-550 <HOY>
A,Coss-references: GB_303734; NID:g205050; PIDN:AAA41472.1; PID:g205051
C,Keywords: transmembrane protein
F,412-536/Domain: C-type lectin homology <LCH>
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                                                                                                                                                                                              || || || || || CAEILSDGLWNDNFCQQVNRWACE 294
                                                                                                                                                                      282 CAHFHPDGRWNDDVCQRPYHWVCE 305
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R.Nakamura, K.; Funakoshi, H.; Miyamoto, K.; Tokunaga, F.; Nakamura, T.
Biochem. Biophys. Res. Commun. 280, 1028-1035, 2001
A;Ttle: Molecular cloning and functional characterization of a human scavenger receptor A;Reference number: JC7595; MUID:21092718; PMID:11162630
A;Contents: Placenta
A;Accession: JC7595
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A;Cross-references: UNIPROT:Q9BYH7; DDBJ:AB038518
C;Comment: This receptor, a member of the scavenger receptor family, belonging to the tyre important role in host defense. It forms a timer and plays a role in recognizing infect, C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;57-112/Domain: extracellular #status predicted <EXT>
F;113-335/Domain: coiled coil #status predicted <COC>
F;369-384/Region: serine-threonine-rich #status predicted
F;459-584/Region: serine-threonine-rich #status predicted <COL>
F;4607-732/Domain: C-type lectin/carbohydrate recognition domain #status predicted <CRD>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      308 SRSNRFTWMGLSDLNQEGTWQWVDGSPLLPSFKQYWNRGEPNN-----VGEEDCAEFSG 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 ODAI-----YONLTOLKAAVGELSEKSKLÖEIYQELTOLKAAVGELPEKSKLOEIYÖELT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----LLRV------NA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 KQQEIYQELTŘLKAAVGELPEKSKQQEIYQELTRLKAAVGELPEKSKQQEIYQELTQLKA 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            175 STEGTC--CPVNWVEHQDSCYWFSHSGMSWAEAEKYCQLKNAHLVVINSREEQNF--VQK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231 YLGSAYTWMGLSD--PEGAWKWVDGTDYATGF-QNWKPGQPDDWQGHGLGGGEDCAHFHP 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73
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C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C;Accession: JC7595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 QTRGYKSLAGCLGHGPLVLQ-----LLSFTLLAGLLVQVSKVPSSISQEQSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 RDLVTLRTDFSNFTSNTVA-----EIQALTSQGSSLEETIASL--KAEVEGFKQE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 KVQGFK-----NGPLPLQSLLQRLRSGPCHLLLSLGL--GLLLLVIICVVGFQNSKFQ
A;Reference number: A46274, MUID:92390446; PMID:1518869
A;Accession: A46274
A;Status: preliminary
A;Molecule type: nucleic acid
A;Molecule type: nucleic acid
A;Residues: 1-404 <CUR>
A;Cross-references: UNIPROT:09NNX6
A;Experimental source: placenta
A;Note: sequence extracted from NCBI backbone (NCBIN:113134, NCBIP:113135)
P;256-377/Domain: C-type lectin homology <LCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
18.2%; Score 316; DB 2; Length 404;
Best Local Similarity 27.1%; Pred. No. 5.3e-18;
Matches 105; Conservative 52; Mismatches 116; Indels 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Map position: 18p11.32
C,Keywords: colled coil; glycoprotein; transmembrane protein
F;1-39/Domain: cytosolic (amino-terminus) #status predicted <CYT>
F;16-19/Region: internalization signal YKRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 -RQAGVSEL-----QEHTTQKAHLGHCPHCPSVCVPVHSEM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;40-56/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            scavenger receptor with C-type lectin type I - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NG-WNDDKCNLAKFWICKKSAASCSRD 387
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for glycoproteins. Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89 OMSONLOELOAEOKOMKAQDSRLSQNLTGLQEDLRNAQSQNSKLSQNLNRLQDDLVNIKS 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EAEKYCQLKNAHLVVINSREEQNFVQKYLGSAYTWMGLSD--PEGAWKWVDGTDYATGFQ 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Gallus gallus (chicken)
C;Date: 08-Oct-1981 #sequence revision 08-Oct-1981 #text_change 09-Jul-2004
C;Date: 08-Oct-1981 #sequence revision 08-Oct-1981 #text_change 09-Jul-2004
C;Date: 08-Oct-1981 #sequence revision 08-Oct-1981 #text_change 09-Jul-2004
C;Date: 08-Oct-1981 #sequence of sequence of sequence of sequence of a membrane receptor for glycoprote:
A;Title: Complete amino acid sequence of a membrane receptor for glycoprote:
A;Reference number: A03167; MUID:81215504; PMID:7240175
A;Accession: A03167
A;Molecule type: protein
A;Rossidues: 1-207 -0DIS
A;Note: some or all of the cysteines are involved in disulfide bonds
Date: 12-Feb-1993 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 LLSTAMWAGLLALLLLWHWETEKNLKQLGDTAIQNVSHVT--KDLQKFQSNQLAQKSQVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMLLRVQQLVQDLXKLTCQVATL----NNNASTEGTCCPVNWVEHQDSCYWFSHSGMSWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42 LLSLGLGLLLLVIICVVGFQNSKFQRDL------VTLRTDFSNFTSNTVAEIQALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 SQGSSLEETIA---SLKAEVEGFKQERQAGVSELQEHTTQKAHLG-HCPHCPSVCVPVHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F,65,114/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            262 NWKPGQPDDWQGHGLGGGEDCAHFHPDGRWNDDVCQRPY--HWVCE 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NWNPGEPNNG-----GOGEDCVMMRGSGOWNDAFC-RSYLDAWVCE 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
16.5%; Score 287; DB 1; Length 33;
Best Local Similarity 28.7%; Pred. No. 9.4e-16;
Matches 82; Conservative 44; Mismatches 128; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'Domain: C-type lectin homology <LCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hepatic lectin - chicken
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A; Residues: 1-309 <FID.
A; Residues: 1-309 <FID.
A; Residues: 1-309 <FID.
A; Cross-references: UNIPROT:063097; EMBL:X73579; NID:9313672; PIDN:CAA51981.1; PID:93136
C; Superfamily: IgE receptor II; C-type lectin homology
C; Keywords: B-cell; glycoprotein; immunoglobulin receptor; macrophage; tandem repeat; tr
F:1-25/Domain: intracellular #status predicted <INT>
F:1-25/Domain: intracellular #status predicted <INT>
F:24-809/Domain: extracellular #status predicted <EXT>
F:26-309/Product: soluble IgE-binding factor (29K) #status predicted <IGI>F:149-209/Product: soluble IgE-binding factor (25-27K) #status predicted <BF:>F:164-283/Domain: C-type lectin homology <LCH>
F:192-283,260-274/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gauchat, J.F.; Ayal
                                                                                                                                                                                                                                                                                                                                                                                                                                              IgE Fc receptor II, low-affinity - rat
NyAlternate names: CD23; lymphocyte IgE receptor
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S34198
R;Plorese Romo, L.; Shield, J.; Humbert, Y.; Graber, P.; Aubry, J.P.; Gauchat, J.F.; Aya submitted to the EMBL Data Library, June 1997
A;Description: Inhibition of an in vivo antigen-specific IgE response by antibodies to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      268
                                                                                           177 EGTCCPVNWVEHQDSCYWFSHSGMSWAEAEKYCQLKNAHLVVINSREEQNFVQKYL-GSA 235
                                                                                                                      603 EDNSCPPHWKNFTDKCYYFSVEKEIFEDAKLFCEDKSSHLVFINTREEQQMIKKQMVGRE 662
                                                                                                                                                                                       236 YTWMGLSDP--EGAWKWVDGTDYATGFQNWKPGQPDDWQGHGLGGGEDCAHFHPDGRWND 293
                                                                                                                                                                                                               89 LSQNLNELQEDLINVKSQN----SELSQNLNTLQED------LVNVKSQGLNEKR 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155 QLVQDLKKLTCQVATL----NNNASTEGTCCPVNWVEHQDSCYWPSHSGMSWAEAEKYCQ 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97 LEETIASLKAEVEGFKQERQAGVSELQE--HTTQKAHLGHCPHCPSVCVPVHSEMLLRVQ 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29 VGLLTTVMVWLLALLLLMHWETEKSLKQLGDAAIQNALQMSQNLEELQAEQKQMKSQDSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47 LGLL-----LLVIICVVGFQNSKFQRDLVTLRTDFSNFTSNTVAEIQA----LTSQGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      211 LKNAHLVVINSREEQNFVQKYLGSAYTWMGLSD--PEGAWKWVDGTDYATGFQNWKPGQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IGE Fc receptor, low-affinity - mouse N;Alternate names: Blast-2; CD23; Fc-epsilon-RII; lymphocyte IgE receptor C;Species: Mus musculus (house mouse)
                                                 . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 309;
18.0%; Score 313; DB 2; Length 742; 43.9%; Pred. No. 1.9e-17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             269 DDWQGHGLGGGEDCAHFHPDGRWNDDVCQRPY--HWVCE 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
16.6%; Score 288.5; DB 1;
Best Local Similarity 29.0%; Pred. No. 6.5e-16;
Matches 81; Conservative 47; Mismatches 108;
                                            26; Mismatches
                                                                                                                                                                                                                                                                                     294 DVCQRPYHWVCE 305
                                                                                                                                                                                                                                                                                                                |: :::||
720 FQCEDVNNFICE 731
                                          Conservative
                   Similarity
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                                               58,
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Query Match
                   Best Local
Matches 5
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A,Note: all exon sequences were determined but the complete sequence is not shown R;Matsui, M.; Nunez, R.; Sachi, Y.; Lynch, R.G.; Yodoi, J.
FEBS Lett. 335, 51-56, 1992
A;Title: Alternative transcripts of the human CD23/Fc-epsilon-RII. A possible novel mech?
A;Reference number: S39442; MUID:94063078; PMID:8243664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: A26164
A;Molecule type: mRNA
A;Residues: 1-266, TT, 270-321 <LUD>
A;Cross-treferences: GB:X04772; NID:g34002; PIDN:CAA28465.1; PID:g34003
A;Cross-treferences: GB:X04772; NID:g34002; PIDN:CAA28465.1; PID:g34003
A;Cross-treferences: GB:X04772; NID:g34002; PIDN:CAA28465.1; PID:g34003
A;Note: part of this sequence, including the amino end of soluble forms of the protein, v
R;Ikuta, K; Takami, M.; Kim, C.W.; Honjo, T.; Miyoshi, T.; Tagaya, Y.; Kawabe, T.; Yodos
Proc. Natl. Acad. Sci. U.S.A. 84, 819-823, 1987
A;Title: Human lymphocyte Fr receptor for IgE: sequence homology of its cloned cDNA with A;Reference number: A26589; MUID:87118255; PMID:2949326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-321 < IKU>
A; Residues: 1-321 < IKU>
A; Crose-references: GBMI5059; NID:g182447; PIDN:AAA52434.1; PID:g182448
A; Crose-references: GBMI5059; NID:g182447; PIDN:AAA52434.1; PID:g182448
A; Crose-references: GBMI5059; NID:g182447; PIDN:AAA52434.1; PID:g182448
A; Note: part of this sequence, including the amino end of soluble forms of the protein, v
R; Yokota, A.; Kikutani, H.; Tanaka, T.; Sato, R.; Barsumian, E.L.; Suemura, M.; Kishimotc
Cell 55, 611-618, 198
A; Title: Two species of human Fc-epsilon receptor II (Fc-epsilon-RII/CD23): tissue-specif
A; Reference number: A31924; MUID:89028672; PMID:2972386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 'MNPBSO', 8-14 < YOK>
A; Crost-references: GB:M23562; NID:g182444
A; Crost-references: GB:M23562; NID:g182444
A; Experimental source: splice form IIb
R; Letellier, M.; Sarfati, M.; Delespesse, G.
MOI. Immunol. 26, 1105-1112, 1989
A; Title: Mechanisms of formation of IgE-binding factors (soluble CD23)-I. Fc epsilon R II)
A; Reference number: JL0132; MUID:90220658; PMID:2534424
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A;Contents annotation; conformation by theoretical model, residues 173-285
C;Comment: The sequence of the splice form a is shown.
C;Comment: This receptor for the Fc portion of IgE is expressed in various hematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein
A; Residues: 1-321 < LET>
A; Esterimental source: lymphoblastoid B cell line
A; Experimental source: lymphoblastoid B cell line
B; Rose, K.; Turcatti, G; Graber, P.; Pochon, S.; Regamey, P.O.; Jansen, K.U.; Magnenat,
Biochem. J. 286, 819-824, 1992
A; Title: Partial characterization of natural and recombinant human soluble CD23.
A; Ritle: Partial characterization of natural and recombinant human soluble CD23.
A; Recession: S29107
A; Molecule type: protein
A; Residues: 152-166;173-179;189-212;230-263;268-306 < ROS>
B; Padlan, E.A.; Helm, B.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D.; Kilchherr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Cloning and expression of the cDNA coding for a human lymphocyte IgB receptor. A;Reference number: A26164; MUID:87218454; PMID:3034567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C, Comment: Splice form a is expressed constitutively in B-cells; b is expressed in C, Comment: Soluble IgE-binding factors are produced by proteolytic cleavage of IgE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Contents: annotation; conformation by theoretical model, residues 173-285
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: S39443
A;Molecule type: DNA
A;Residues: 'MNPPSQD', 47-50 <MAS2>
A;Experimental Source: splice form b'
R;Ludin, C.; Hoferetter, H.; Sarfati, M.; Levy, C.A.; Suter, U.; Alaimo,
EMBO J. 6, 109-114, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the Brookhaven Protein Data Bank, November 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Cross-references: GDB:118888; OMIM:151445
A; Map position: 19p13.3-19p13.3
                                                                                                                                                                                                                                                                  A, Accession: S39442
A, Molecule type: DNA
A, Residues: 1-7,'D', 47-50 cMAS1>
A, Experimental source: splice form a'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: GDB:FCER2; FCE2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: JL0132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession: A26589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: A31924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Bajorath, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :Genetics:
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A; Accession: A2667
A; Molecule type: mRNA
A; Experimental source: EBV-transformed B lymphoblastoid cells RPMI-8866
A; Experimental source: EBV-transformed B lymphoblastoid cells RPMI-8866
B; Suter, U.; Bastos, R.; Hofsterter, H.
Nucleic Acids Res. 15, 7295-7308, 1987
A; Title: Molecular structure of the gene and the 5'-flanking region of the human lymphoc
A; Title: Molecular structure of the gene and the 5'-flanking region of the human lymphoc
A; Reference number: S03279; MUID:88015596; PMID:2958779
A; Status: nucleic acid sequence not shown; not compared with conceptual translation
A; Residues: 157-284
A; Cross-references: GB:X06049; NID:931316
     A;Note: residues 24-48 form an uncharged, hydrophobic region that may interact with or e R;Mellow, T.E.; Halberg, D.; Drickamer, K. J. Blol. Chem. 263, 5468-5473, 1988 A;Blol. Chem. 263, 5468-5473, 1988 A;Title: Endocytosis of N-acetylglucosamine-containing glycoproteins by rat fibroblasts A;Reference number: A28194; MUID:88186849; PMID:3281941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Cross-references: GB:M63225, GB:M63226, GB:M63227, GB:M63228, GB:M63229, GB:M63230, NJ
C;Comment: Hepatic lectin is a membrane receptor protein that recognizes and binds expos
                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:J03188; NID:g212246; FIDN:AAA48937.1; FID:g212247
R;Bezouska, K.; Crichlow, G.V.; Rose, J.M.; Taylor, M.E.; Drickamer, K.
Biol. Chem. 266, 11604-11609, 1991
A;Title: Evolutionary conservation of intron position in a subfamily of genes encoding A;Reference number: A40427; MUID:91268022; PMID:2050668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IgE Fc receptor II, low-affinity [validated] - human N;Alternate names: Blast-2; CD23; Fc-epsilon-RII; lymphocyte IgE receptor N;Contains: IgE Fc receptor II, splice form a; IgE Fc receptor II, splice form c; IgE C;Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Date: 31. Mar-1988 #sequence revision 31-Mar-1988 #text change 09-Jul-2004
C;Accession: A26067; S03279; $39442; S39443; A26164; A26589; A31924; JL0132; S29107
R;Kikutuani, H.; Inui, S.; Sato, R.; Barsumian, E.L.; Owaki, H.; Yamasaki, K.; Kaisho, A;Ill 47, 657-665, 1986
A;Title: Molecular structure of human lymphocyte receptor for immunoglobulin E.
A;Reference number: A26067; MUID:87051737; PMID:2877743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 SEMLLRVQQLVQDLKKLTCQVATLNNNASTEGTCCPV----NWVEHQDSCYWFSHSGMS 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44 SVSLARIAALSSKLS--TLQSEPKHNFSSRDSLLFPCGAQSRQWEYFEGRCYYFSLSRMS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         202 WAEAEKYCOLKNAHLVVINSREEQNFVQKYLGSAYTWMGLSD--PEGAWKWVDGTDYATG 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aintrons: 15/1; 50/1; 75/1; 125/3; 163/2
C; Superfamily: hepatic lectin; C-type lectin homology
C; Superfamily: hepatic lectin; C-type lectin; lectin; transmembrane protein
C; Keywords: acetylated amino end; glycoprotein; lectin; transmembrane predicted <IMI>
F; 1-23/Domain: intracellular #status predicted <IMI>
F; 24-47/Domain: extracellular #status predicted <IMI>
F; 78-201/Domain: c-type lectin homology <ICH>
F; 78-201/Domain: c-type lectin homology <ICH>
F; 78-201/Domain: acetylated amino end (Met) #status experimental
F; 67/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-207 <MEL>
A;Cross-references: GB:J03188; NID:g212246; PIDN:AAA48937.1; PID:g212247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      260 FQNWKPGQPDDWQGHGLGGGEDCAHFHPDGRWNDDVCQRPYHWVCEAGL 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 FTFWKEGEPIN----RGFNEDCAHVWTSGQWNDVYCTYECYYVCEKPL 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
16.2%; Score 281; DB 1; Length 207; Best Local Similarity 36.7%; Pred. No. 1.6e-15; Matches 62; Conservative 26; Mismatches 67; Indels 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-207 <BEZ>
                                                                                                                                                                                                                                                                        A; Accession: A28194
A; Molecule type: mRNA
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δ g ઠે 셤 ò 셤 other Fc rec

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A;Introns: 8/1; 46/1; 64/1; 85/1; 106/1; 127/1; 157/1; 207/3; 243/2
C;Superfamily: IgE receptor II; C-type lectin homology
C;Superfamily: IgE receptor II; C-type lectin homology
C;Keywords: alternative splicing; B-c=l; glycoprotein; immunoglobulin receptor; macroph
F; MNPPSQD', 47-321/Product: IgE Fc receptor II, splice form b #status predicted cSFB>
F;1-321/Product: IgE Fc receptor II, splice form b #status predicted cSFB>
F;1-321/Product: IgE Fc receptor II, splice form a #status predicted cSFB>
F;1-23/Domain: intracellular #status predicted cTMT>
F;1-27, D', 47-321/Product: IgE Fc receptor II, splice form a' #status predicted cSFA>
F;1-27, D', 47-321/Product: IgE Fc receptor II, splice form a' #status predicted cSFAI>
F;1-27, D', 47-321/Product: IgE Fc receptor II, splice form a' #status predicted cSFAI>
F;1-27, D', 47-321/Product: IgE Fc receptor II, splice form a' #status predicted cSFAI>
F;1-27, D', 47-321/Product: Soluble IgE-binding factor (37K) #status predicted cIGE>
F;6-1-31/Product: Soluble IgE-binding factor (25-27K), short form #status experimental
F;10-221/Product: Soluble IgE-binding factor (25-27K), short form #status experimental
F;13-221/Product: Soluble IgE-binding factor (25-27K), short form #status experimental
F;13-221/Product: Soluble IgE-binding factor (25-27K), short form #status experimental
F;13-221/Product: Soluble IgE-binding factor (25-27K), short form #status F;147-148/Cleavage site: Lys-Leu (unidentified proteinase) #status experimental
F;147-148/Cleavage site: Arg-Met (unidentified proteinase) #status experimental
F;149-150/Cleavage site: Arg-Met (unidentified proteinase) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QNSKFQRDLVTLRTDFSNFTSNTVAEIQALTSQGSSLEETIASLKAEVEGFKQERQAGVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELQEHTTQKAHLGHCPHCPSVCVPVHSEMLLRVQQLVQDLKKLTCQVATLANNASTEGTC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 ELNERNEA------MELQVSSGFVC 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -- CPVNWVEHQDSCYWFSHSGMSWAEAEKYCQLKNAHLVVINSREEQNFVQKYLGSAYTW 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161 NTCPEKWINFQRKCYYPGKGTKQWVHARYACDDMEGQLVSIHSPEEQDFLJFKHASHTGSW 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         239 MGLS--DPEGAWKWVDGT--DYATGPQNWKPGQPDDWQGHGLGGGEDCAHFHPDGRWNDD 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                221 IGLRNLDLKGEFIWVDGSHVDYS----NWAPGEPT----SRSQGEDCVMMRGSGRWNDA 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 QSTQISQELEELR-----AEQQRLKSQDLELSWNINGLQADLSSFKSQ----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 15.8%; Score 274.5; DB 1; Length 321; Best Local Similarity 29.4%; Pred. No. 9.4e-15; Matches 74; Conservative 32; Mismatches 87; Indels 59
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Sequence 28, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 21, Appl

Sequence 2,

Sequence 28, A Sequence 219, A Sequence 21, A S

Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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BLOEHTTOKAHLGHCPHCPSVCVPVHSEMLLRVQQLVQDLKKLTCQVATLNNNASTEGTC 180
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Breint No. US/2020165346A1

GENERAL INFORMATION:
APPLICANT: Schering-Plough Corporation
APPLICANT: Schering-Plough Corporation
APPLICANT: Schering-Plough Corporation
APPLICANT: Schering-Plough Corporation
TITLE OF INVENTION: MAWMALIAN MEMBRANE PROTEIN GENES; RELATED REAGENTS
FILE REFERENCE: SF06598
CURRENT APPLICATION NUMBER: US/09/862,802
CURRENT APPLICATION NUMBER: US 09/111,470
PRIOR APPLICATION NUMBER: US 09/111,470
PRIOR APPLICATION NUMBER: US 09/111,470
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 4

LENGTH: 316
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100.0%; Pred. No. 3.1e-151;
tive 0; Mismatches 0;
US-10-236-392-8

US-10-236-392-6

US-10-072-012-513

US-10-262-8139-94

US-10-151-274-1

US-10-1151-274-1

US-10-184-150-1

US-10-184-150-1

US-10-1328-997-1

US-10-223-084-28

US-10-223-084-28

US-10-223-087-28

US-10-223-081-28

US-10-233-081-28

US-10-233-081-28

US-10-233-081-28

US-10-233-081-28

US-10-245-763-219

US-10-203-860-24

US-10-203-860-24

US-10-203-860-25

US-10-203-860-25

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US-10-203-801-895-2012-160
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     Best Local Similarity 100.0
Matches 316; Conservative
                                                                                                                                                                                                                                                                                                                 342
457
542
   TYPE: PRT
ORGANISM: Unknown
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   JS-09-862-802-4
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Sequence 13, Appl
Sequence 12, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 8, Appli
Sequence 5, Appli
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762.317 Million cell updates/sec
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                                                                                                                                                                             US-10-829-107-4
1738
1 MTRTYENFQYLENKVKVQGF......QRPYHWVCEAGLGQTSQESH 316
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1: \cgn2 \( \) \cgn2 \( \
                                                                                                                 May 27, 2005, 12:44:49 ; Search time 143 Seconds
               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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5 US-10-138-588-90

6 US-10-829-107-13

6 US-10-829-107-12

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6 US-10-829-107-10

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                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                               Gapop 10.0 , Gapext 0.5
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1738
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49 6400 6 8 6 11 2 11

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JUNEARLIANTION: INTOKARILLON:

JUNEARLIANTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES, NUCLEIC ACI
TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES, NUCLEIC ACI
TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
TILE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
CURRENT APPLICATION NUMBER: US/10/138,588

PRIOR FILING DATE: 2001-05-03

PRIOR PILING DATE: 2001-06-17

PRIOR APPLICATION NUMBER: 60/324,757

PRIOR PILING DATE: 2001-08-25

PRIOR PILING DATE: 2001-08-25

PRIOR FILING DATE: 2001-05-04

PRIOR PILING DATE: 2001-05-04

PRIOR FILING DATE: 2001-05-04

NUMBER OF SEQ ID NOS: 203

SEQ ID NO 90

LENGTH: 319
300
                                                                                                                                                                                                                                                 241 LSDPEGAWKWVDGTDYATGFQNWKPGQPDDWQGHGLGGGGDCAHFHPDGRWNDDVCQRPY 300
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                                                                                                                             181 CPVNWVEHQDSCYWFSHSGMSWAEAEKYCQLKNAHLVVINSREEQNFVQKYLGSAYTWMG
                                                                                                                                                                                                                    LSDPEGAWKWVDGTDYATGFQNWKPGQPDDWQGHGLGGGGEDCAHFHPDGRWNDDVCQRPY
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98.9%; Score 1718.5; DB 19
Best Local Similarity 98.7%; Pred. No. 1.9e-149;
Matches 315; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-138-588-90
, Sequence 90, Application US/10138588
; Publication No. US20040018594A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                        HWVCEAGLGQTSQESH 316
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US-10-138-588-90
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NAME/KEY: misc_feature
LOCATION: (775)..(776)
OTHER INFORMATION: ASGPRm (Table 2) has sequence insert encoding GEE between nucleot
OTHER INFORMATION: ides 775-776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEX: misc_feature
LOCATION: (1064).
OTHER INFORMATION: nucleotide 1064 of DCMP2s may be A, which would encode Asn rather
OTHER INFORMATION: than Asp at the residue numbered 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/10829107

Sequence 4, Application US/10829107

Publication No. US20040192892A1

GENERAL INFORMATION:

APPLICANT: Valladeau, Jenny

APPLICANT: Bates, Elizabeth Ester Mary

APPLICANT: Lebecque, Sem

TITLE OF INNENTION: Isolated Mammalian Membrane Protein Genes; Related Reagents

TITLE OF INNENTION ISOlated Mammalian Membrane Protein Genes; Related Reagents

FILE REPREBNCE: SF0695 B

CURRENT APPLICATION NUMBER: US/10/829,107

CURRENT FILING DATE: 2001-05-22

PRIOR PILING DATE: 1999-07-09

PRIOR PILING DATE: 1999-07-09

PRIOR PILING DATE: 1999-07-08

NUMBER OF SEQ ID NOS: 13

SEQ ID NO 4

LENGTHRES PATENTIN VERSION 3.1

SEQ ID NO 4

LENGTHRES DATE: DATE
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                                                              CPVNWVEHQDSCYWFSHSGMSWAEAEKYCQLKNAHLVVINSREEQNFVQKYLGSAYTWMG 240
                                                                                                 CPVNWVEHQDSCYWFSHSGMSWAEAEKYCQLKNAHLVVINSREEGNFVQKYLGSAYTWMG 240
                                                                                                                                                                                     LSDPEGAWKWVDGTDYATGFQNWKPGQPDDWQGHGLGGGEDCAHFHPDGRWNDDVCQRPY 300
                                                                                                                                                                                                                    241 LSDFEGAWKWYDGTDYATGPQNWKPGQPDDWQGHGLGGGGBDCAHFHPDGRWNDDVCQRPY 300
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      121 ELQEHTTQKAHLGHCPHCPSVCVPVHSEMLLRVQQLVQDLKKLTCQVATLNNNASTEGTC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (608)..(673)
OTHER INFORMATION: short form lacks nucleotides 608-673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: mammalian nucleic acid and protein
                                                                                                                                                                                                                                                                                                                                                        301 HWVCEAGLGQTSQESH 316
                                                                                                                                                                                                                                                                                                         301 HWVCEAGLGQTSQESH 316
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; OTHER INFORMATION: mammalian protein (ASGPRm is a macrophage derived ASGPR)
US-10-829-107-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 QNSKFQRDLVTLRTDFSNFTSNTVAEIQALTSQGSSLEETIASLKAEVEGFKQERQA--- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 GTCCPVNWVEHQDSCYWFSHSGMSWAEAEKYCQLKNAHLVVINSREEQNFVQKYLGSAYT 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 WMGLSDPEGAWKWVDGTDYATGFQNWKPGQPDDWQGHGLGGGEDCAHFHPDGRWNDDVCQ 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 QNSKFQRDLVTLRTDFSNFTSNTVAEIQALTSQGSSLEETIASLKAEVEGFKQERQAGVS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MTRIYENFQYLENKVKVQGFKNGPLPLQSLLQRLRSGPCHLLLSLGLGLLLLVIICVVGF
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Patent No. US2002016534641

GENERAL INFORMATION:

APPLICANT: Schering-Plough Corporation
TITLE OF INVENTION: MAMMALIAN MEMBRANE PROTEIN GENES; RELATED REAGENTS
PILE REFERENCE: SF06958

CURRENT APPLICATION UNDER: US/09/862,802

CURRENT FILING DATE: 1098-07-08

PRIOR FILING DATE: 1998-07-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 292;
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CURRENT APPLICATION NUMBER: US/10/829,107
CURRENT FILING DATE: 2004-04-21
PRIOR APPLICATION NUMBER: US/09/862,802A
PRIOR FILING DATE: 2001-05-22
PRIOR FILING DATE: 1997-07-09
PRIOR FILING DATE: 1997-07-09
PRIOR FILING DATE: 1997-07-08
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
LENGTH: 292
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 273
TYPE: PRT
ORGANISM: Unknown
FEATURE:
                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Unknown
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                                               Sequence 13, Application US/10829107

Sequence 13, Application US/10829107

Sequence 13, Application No. US20040192892A1

SENERAL INFORMATION:

APPLICANT: Valladeau, Jenny

APPLICANT: Bates, Elizabeth Ester Mary

APPLICANT: Bates, Senge J.E.

APPLICANT: Bates, Ester Mary

APPLICANT: Bates, Senge J.E.

APPLICANT: Saeland, Sem

CURRENT APPLICATION NUMBER: US/10/829,107

CURRENT APPLICATION NUMBER: US 60/053,080

PRIOR PILING DATE: 1997-07-09

PRIOR PILING DATE: 1998-07-08

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn version 3.1

SEQ ID NO 13

LENGTH: 289

LENGTH: 289
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Sequence 12, Application US/10829107

Sequence 12, Application No. US20040192892A1

Sequence 12, Sequence 12, Application No. US20040192892A1

GENERAL INFORMATION:

APPLICANT: Nalladeau, Jenny

APPLICANT: Bates, Elizabeth Ester Mary

APPLICANT: Ford, John

APPLICANT: Lebeque, Serge J.E.

APPLICANT: Applicant Isolated Mammalian Membrane Protein Genes; Related Reagents

TITLE OF INVENTION: Isolated Mammalian Membrane Protein Genes; Related Reagents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , OTHER INFORMATION: mammalian protein (DCMP2 short form)
US-10-829-107-13
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                                 10-829-107-13
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us-10-829-107-4.rapb

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US-10-138-588-88

Sequence 88, Application US/10138588

Sequence 88, Application US/10138588

Publication No. US200400185941

GENERAL INFORMATION:

TITLE OF INVENTION:

FILE OF INVENTION: NOVEL ANTIBEDIES THAT BIND TO ANTIGENIC POLYPEPTIDES, NUCLEIC ACLT

TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE

FILE REFERENCE: 21402-347A

CURRENT APPLICATION NUMBER: 60/288,395

PRIOR PILING DATE: 2001-05-03

PRIOR FILING DATE: 2001-05-03

PRIOR FILING DATE: 2001-08-17

PRIOR PLILING DATE: 2001-08-17

PRIOR PLILING DATE: 2001-08-17

PRIOR PLILING DATE: 2001-09-25

PRIOR FILING DATE: 2001-05-04

NUMBER OF SEQ ID NOS: 203

SERIOR DATE: 2001-05-04

SERIOR PLING DATE: 2001-05-04
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83 TVAEIQALTSQGSSLEETIASLKAEVEGFKQERQAGVSELQEHTTQKAHLGHCPHCPSVC 142
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; APPLICANT: Schering-Plough Corporation
; TITLE OF INVENTION: MAMMALIAN MEMBRANE PROTEIN GENES; RELATED REAGENTS; FILE REFERENCE: SF0695B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263 WKPGQPDDWQGHGLGGGGBDCAHFHPDGRWNDDVCQRPYHWVCEAGLGQTSQESH 316
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Best Local Similarity 89.5%; Pred. No. 3.3e-121;
Matches 263; Conservative 0; Mismatches 4;
                                                                                                                                                                     298 RPYHWVCEAGLGQTSQESH 316
                                                                                                                                                                                                                  255 RPYHWVČEAGLGQTSQESH 273
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US-10-138-588-88
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US-09-862-802-5
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APPLICANT: Lebecque, Serge J.E.
APPLICANT: Saeland, Sem
TITLE OF INVENTION: Isolated Mammalian Membrane Protein Genes; Related Reagents
FILE REFERENCE: SF0695 B
CURRENT APPLICATION NUMBER: US/10/829,107
CURRENT APPLICATION NUMBER: US/09/862,802A
FRIOR PLING DATE: 2001-05-22
PRIOR PLING DATE: 2001-05-22
PRIOR PLING DATE: 1997-07-09
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 13
SEQ ID NOS: 13
SEQ ID NO 10
LENGTH: 273
                                                                                             61 QNSKFQRDLVTLRTDFSNFTSNTVAELQALTSQGSSLEETIASLKAEVEGFKQERQAGVS 120
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                                                                                                                                                                                                                                                                                       178 GTCCPVNWVEHQDSCYWFSHSGMSWAEAEKYCQLKNAHLVVINSREEQNFVQKYLGSAYI 237
                                                                                                                                                                                                                                                                                                                                                                                  238 WMGLSDPEGAWKWVDGTDYATGFONWKPGQPDDWQGHGLGGGEDCAHFHPDGRWNDDVCQ 297
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                                                 41
                                                                                                                      42 QNSKFQRDLVTLRTDFSNFTSNTVAEIQALTSQGSSLEETIASLKAEVEGFKQERQA--- 98
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                                                                                                                                                                                                                      135 GTCCPVNWVEHQDSCYWFSHSGMSWAEAEKYCQLKNAHLVVINSREEGNFVQKYLGSAYT
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  1 MTRIYENPQYLENKVKVQGFKNGPLPLQSLLQRLRSGPCHLLLSLGLGLLLLVIICVVGF
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Pred. No. 9.3e-123;
0; Mismatches 0; Indels 49:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: mammalian nucleic acid and protein US-10-829-107-10
                             1 MIRIYENFQYLENKVKVQGFKNGPLPLQS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/10829107
Publication No. US20040192892A1
GENERAL INFORMATION:
APPLICANT: Valladeau, Jenny
APPLICANT: Ravel, Odile
APPLICANT: Bates, Elizabeth Ester Mary
APPLICANT: Pord, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RPYHWVCEAGLGQTSQESH 316
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Best Local Similarity 84.6%;
Matches 270; Conservative
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US-10-829-107-10
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                                                                                                                        1 MIRIYENFQYLENKVK-VQGFKNGPLPLQSLLQRLRSGPCHLLLSLGLGLLLLVIICVVG
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APPLICANT: SCHERING: NAMMALIAN MEMBRANE PROTEIN GENES; RELATED REAGENTS
TITLE OF INVENTION: MAMMALIAN MEMBRANE PROTEIN GENES; RELATED REAGENTS
FILE REFERENCE: 2002-01-10
CURRENT APPLICATION NUMBER: US/09/862,802
FURRENT FILING DATE: 2002-01-10
PRIOR PELLING DATE: 1998-07-08
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 6
LENGTH: 287
                                                                            Gaps
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                                                                            29;
                           Query Match 53.1%; Score 923.5; DB 16; Length 291; Best.Local Similarity 54.6%; Pred. No. 2.4e-76; Matches 172; Conservative 47; Mismatches 67; Indels 29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: mammalian protein US-09-862-802-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/09862802; Patent No. US20020165346A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300 YHWVCEAGLGQTSQE 314
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ORGANISM: Unknown
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APPLICANT: Lebecque, Serge J.E.
APPLICANT: Saeland, Sem
TITLE OF INVENTION: ISolated Mammalian Membrane Protein Genes; Related Reagents
FILE REFERENCE: S70695 B
CURRENT APPLICATION NUMBER: US/10/829,107
CURRENT FILING DATE: 2004-04-21
PRIOR FILING DATE: 1997-07-09
PRIOR FILING DATE: 1997-07-09
PRIOR FILING DATE: 1997-07-08
NUMBER OF SEQ ID NOS: 13
SOGTWARR: Patentin version 3.1
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CURRENT APPLICATION NUMBER: US/09/862,802
CURRENT FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 09/111,470
PRIOR FILING DATE: 1998-07-08
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 291
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; OTHER INFORMATION: mammalian protein
US-10-829-107-5
                                                                                                                                                                                                                                         FEATURE:
, OTHER INFORMATION: mammalian protein US-09-862-802-5
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Best Local Similarity 54.6
Matches 172; Conservative
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ORGANISM: Unknown
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LENGTH: 291
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US-10-829-107-5
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APPLICANT: Valladeau, Jenny
APPLICANT: Ravel, Odile
APPLICANT: Bates, Elizabeth Ester Mary
APPLICANT: Bates, Elizabeth Ester Mary
APPLICANT: Bates, Elizabeth Ester Mary
APPLICANT: Ford, John
APPLICANT: Ford, John
APPLICANT: Saeland, Sem
TITLE OF INVENTION: Isolated Mammalian Membrane Protein Genes; Related Reagents
TITLE OF INVENTION: Isolated Mammalian Membrane Protein Genes; Related Reagents
FILE REFERENCE: S10695 B
CURRENT FILING DATE: 2004-04-21
FRIOR APPLICATION NUMBER: US/99/862,802A
FRIOR APPLICATION NUMBER: US 60/053,080
FRIOR APPLICATION NUMBER: US 60/053,080
FRIOR APPLICATION NUMBER: US 09/111,470
FRIOR FILING DATE: 1998-07-08
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 287
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46.6%; Pred. No. 2e-63;
ive 50; Mismatches 89; Indels 2
                                                                     45.1%; Score 783; DB 15; Length 26
46.6%; Pred. No. 2e-63;
tive 50; Mismatches 89; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 HWVCEAGLGQTSQ 313
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Best Local Similarity 46.64
Matches 146; Conservative
                                                                        Query Match
Best Local Similarity 46.6'
Matches 146; Conservative
  ; ORGANISM: Homo sapiens
US-10-236-392-10
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APPLICANT: Shenoy, Suresh
APPLICANT: Shimkets, Richard A
APPLICANT: Shithson, Glennda
ATTLE OF INVENTION: THEAPBUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-442A
CURRENT APPLICATION NUMBER: US/10/236,392
CURRENT FILING DATE: 2002-09-06
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SOFTWARE: Custom
SEQ ID NO 10
LENGTH: 287
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PRIOR APPLICATION NUMBER: US09/540,763
PRIOR PELING DATE: 2000-03-30
PRIOR PELING DATE: 2000-03-30
PRIOR PELING DATE: 2000-06-19
PRIOR FILING DATE: 2000-06-19
PRIOR FILING DATE: 2000-06-10
PRIOR FILING DATE: 2000-08-10
PRIOR PILING DATE: 2000-08-10
PRIOR PILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: US60/357,303
PRIOR PILING DATE: 2000-09-12
PRIOR FILING DATE: 2002-04-02
PRIOR PILING DATE: 2002-04-02
PRIOR PILING DATE: 2002-04-02
PRIOR PILING DATE: 2000-09-12
PRIOR PELING DATE: 2000-09-07
PRIOR PELING DATE: 2001-09-07
                                                                                                                                                                                                                                                                                                      APPLICANT: Anderson, David W
APPLICANT: Boldog, Ferenc L
APPLICANT: Burgess, Catherine, B
APPLICANT: Catterton, Elina
APPLICANT: Chapoval, Andrei
APPLICANT: Chapoval, Andrei
APPLICANT: Chapoval, Andrei
APPLICANT: Bdinger, Shlomit, R
APPLICANT: Bdinger, Shlomit, R
APPLICANT: Gerlach, Valerie
APPLICANT: Gorman, Linda
APPLICANT: Gresse, William M
APPLICANT: Gueev, Vladamir
                                                                                                                                                                                                                                          Sequence 10, Application US/10236392
Publication No. US20040067490A1
GENERAL INFORMATION:
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LaRochelle, William J
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Malyankar, Uriel M
Miller, Charles E
Millet, Isabelle
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Reiger, Daniel K
Rothenberg, Mark E
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Pena, Carol A
                                                                        301 HWVCEAGLGQTSQ 313
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99 SSSTLTEVQAISTHGGSVGDKITSLGAKLEKQQQDLKA-----DHDALLFHLKHFP--- 149
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                                                                                                                                                                                                                                                                                                                                                                                                                       28; Gaps
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PRIOR FILING DATE: 2001-09-07
PRIOR PILING DATE: 2001-09-07
PRIOR FILING DATE: 2001-09-07
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 794
SOFTWARE: Custom
SEQ ID NOS: 0.00
                                                                                                                                                                                                                                                                                                                                                                Length 306;
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48.3%; Pred. No. 2.8e-61;
ative 44; Mismatches 80;
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Grosse, William M
Gusev, Vladamir
Kekuda, Ramesh
LaRochelle, William J
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Publication No. US20040067490A1
GENERAL INFORMATION:
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Casman, Stacie J
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Chapoval, Andrei
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Edinger, Shlomit, R
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Malyankar, Uriel M
Miller, Charles E
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Reiger, Daniel K
Rothenberg, Mark E
Shenoy, Suresh
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Pena, Carol A
     2000-09-12
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Gerlach, Valerie
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Best Local Similarity 48.3
Matches 142; Conservative
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  FILING DATE: 2000-03
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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...09, Mark E
...09, Suresh shinkets, Richard A
...07, Suresh shinkets, Richard A
...07: Smithson, Glennda
...07: Smithson, Mumber: US09-156
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-----VDLRFVACQMELLHSNGS-QRTC 152
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                                                                                                                                                                                                                                                                                          213 LTDSDGSWKWYDGTDYRHNYKNWAVTQPDNWHGHELGGSEDCVEVQPDGRWNDDFCLQVY 272
                                                      121 ELQEHTTQKAHLGHCPPCPSVCVPVHSEMLLRVQQLVQDLKKLTCQVATLNNNASTEGTC 180
61 QSAQLQAELRSLKEAFSNFSSSTLTEVQAISTHGGSVGDKITSLGAKLEKQQQDLKA--- 117
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APPLICATION NUMBER: US60/367,753
TLING DATE: 2002-03-25
APPLICATION NUMBER: US60/369,479
FILING DATE: 2002-04-02
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APPLICATION NUMBER: US09/659,634
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Malyankar, Uriel M
Miller, Charles E
Miller, Igabelle
Padigaru, Muralidhara
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Publication No. US20040067490A1
GENERAL INFORMATION:
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LaRochelle, William J
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Ellerman, Karen
Gerlach, Valerie
Gorman, Linda
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APPLICANT: Boldog, Ferenc L
APPLICANT: Burgess, Catherine,
APPLICANT: Casman, Stacie J
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Gusev, Vladamir
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Chapoval, Andrei
Crabtree, Julie
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FILE REFERENCE: 21402-442A

CURRENT APPLICATION WUMBER: US/10/236,392

FILE REFERENCE: 21402-442A

FILE REFERENCE: 21402-442A

CURRENT PILING DATE: 2002-0-06

FRIOR APPLICATION NUMBER: US69/540,763

FRIOR APPLICATION NUMBER: US60/390,155

FRIOR PILING DATE: 2000-03-30

FRIOR PELING DATE: 2000-03-30

FRIOR PELING DATE: 2000-03-10

FRIOR PELING DATE: 2000-03-10

FRIOR PELING DATE: 2000-08-10

FRIOR APPLICATION NUMBER: US60/318,765

FRIOR APPLICATION NUMBER: US60/318,765

FRIOR APPLICATION NUMBER: US60/369,479

FRIOR APPLICATION NUMBER: US60/369,479

FRIOR PELING DATE: 2002-03-25

FRIOR APPLICATION NUMBER: US60/369,479

FRIOR APPLICATION NUMBER: US60/318,120

FRIOR FILING DATE: 2000-09-12

FRIOR FILING DATE: 2001-09-12

FRIOR FILING DATE: 2001-09-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 794 SOFTWARE: Custom
Smithson, Glennda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-236-392-6
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Search completed: May 27, 2005, 12:52:11 Job time : 145 secs

Perfect score:

Run on:

Scoring table: Sequence:

Searched:

Database

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Sequence 4, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 10, Appl
Patent No. 5514582
Sequence 10, Appl
Sequence 377, Appl
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APPLICANT: Valladeau, Jenny
APPLICANT: Valladeau, Jenny
APPLICANT: Valladeau, Jenny
APPLICANT: Bates, Elizabeth B.M.
APPLICANT: Lebecque, Serge J.E.
TITLE OF INVENTION: Mammalian Membrane Protein Genes;
TITLE OF INVENTION: Mammalian Membrane Protein Genes;
TITLE OF INVENTION: Mammalian Membrane
ADDRESSEE: BLORESS: 11
CONRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CUTY: Palo Alto
STATE: California
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 60/053,080
FILING DATE: 09-JUL-1998
CLASSIFICATION NUMBER: US 60/053,080
FILING DATE: 09-JUL-1997
ATTORNEY/AGENT INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: 34,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1738; DB 3;
Pred. No. 1e-167;
                                                                                                                                                                                                               US-09-905-125A-377
US-09-902-775A-377
US-09-906-700-377
                                                                                                                                                                           US-08-365-103B-8
US-09-907-794A-377
                                                                                                                                                                                                                                                                   US-09-903-603A-377
US-09-904-920A-377
                               US-08-365-103B-4

US-08-365-103B-6

US-09-535-521-2

US-09-535-521-2

US-09-535-521-5

US-08-535-521-20

5514582-18
                                                                                                                                                            US-08-365-103B-10
                                                                                                                                                                                                                                                                                                       US-09-909-064-377
                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/09111470 Patent No. 6277959 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 316 amino acida TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-09-111-470-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
US-09-111-470-4
Sequence 10, Appl
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 962, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 961, Appli
Sequence 10, S514582
Patent No. 5514582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 13, Appl
Sequence 4, Appli
Sequence 12, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 5, Appli
Sequence 5, Appli
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Sequence 10, Appl
Patent No. 5514582
                                                                                                                     May 27, 2005, 12:44:45 ; Search time 22 Seconds (without alignments) 1072.232 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, 1
Sequence 13,
                                                                                                                                                                                                                              1 MTRIYENFQYLENKVKVQGF.....QRPYHWVCEAGLGQTSQESH 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
Patent No.
Patent No.
Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-111-470-4
US-09-862-802A-4
US-09-862-802A-13
US-08-113-788-4
US-09-113-788-4
US-09-113-788-4
US-09-862-802A-10
US-09-111-470-10
US-09-862-802A-5
US-09-111-470-6
US-09-949-016-9962
US-09-949-016-9961
US-09-949-016-9961
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US-09-531-056A-21
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PCT-US95-04258-10
                                                                                                                                                                                                                                                                                                                                                         Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                       513545 seqs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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1738
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Match Length
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Result

783 745.5 520 520 488 484 454 432 432 432 454 410 410

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## Sequence 13, Application US/09862802A

## Sequence 13, Application US/09862802A

## Sequence 13, Application US/09862802A

## Sequence 13, Application

## APPLICANT: Valladeau, Jenny

## APPLICANT: Ravel, Odile

## APPLICANT: Bates, Elizabeth Ester Mary

## APPLICANT: Bates, Elizabeth Ester Mary

## APPLICANT: Sealand, Sem

## APPLICANT: Sealand, Sem

## TITLE OF INVENTION: Isolated Mammalian Membrane Protein Genes; Related Reagents

## APPLICANT: Sealand, Sem

## TITLE OF INVENTION: Isolated Mammalian Membrane Protein Genes; Related Reagents

## APPLICANT: Sealand, Sem

## TITLE OF INVENTION: Isolated Mammalian Membrane Protein Genes; Related

## APPLICANT: Sealand, Sem

## TITLE OF INVENTION: UNDER: US/09/862,802A

## TITLE OF INVENTION NUMBER: US 09/053,080

## RIOR APPLICATION NUMBER: US 09/111,470

## PRIOR PILING DATE: 1998-07-08

## NUMBER OF SEQ ID NOS: 13

## SEQ ID NO 13

## SEQ ID NO 13

## ENGTH: 289

## CENGTH: 289
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                                                                                                                                                                                                                                                                                       121 BLOEHTTOKAHLGHCPHCPSVCVPVHSEMLLRVQQLVQDLKKLTCQVATLNNNASTEGTC
                                                                                                                                                                                                                                                                                                                                  CPVNWVEHQDSCYWFSHSGMSWAEAEKYCQLKNAHLVVINSREEQNFVQKYLGSAYTWMG
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89.2%; Score 1550.5; DB 4; Length 289;
Best Local Similarity 91.1%; Pred. No. 9.4e-149;
Matches 288; Conservative 1; Mismatches 0; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: mammalian protein (DCMP2 short form)
US-09-862-802A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HWVCEAGLGQTSQESH 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Unknown
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NAME/KEY: misc feature
LOCATION: (775)...(776)
OTHER INFORMATION: ASGREM (Table 2) has sequence insert encoding GEE between nucleot
OTHER INFORMATION: ides 775-776
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APPLICANT: Ravel, Odile
APPLICANT: Bates, Elizabeth Ester Mary
APPLICANT: Bates, Colle
APPLICANT: Bates, John
APPLICANT: Salend, John
APPLICANT: Saeland, Sem
TITLE OF INVENTION: Isolated Mammalian Membrane Protein Genes; Related Reagents
FILE REFERENCE: S76055 B
CURRENT APPLICATION NUMBER: US/09/862,802A
PRIOR APPLICATION NUMBER: US 60/053,080
PRIOR FILING DATE: 1997-07-09
PRIOR PLING DATE: 1997-07-09
PRIOR APPLICATION NUMBER: US 09/111,470
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                                                           MTRTYENFQYLENKVKVQGFKNGPLPLQSLLQRLRSGPCHLLLSLGLGLLLLVIICVVGF
                                                                                                                                                                                        QNSKFQRDLVTLRTDFSNFTSNTVAEIQALTSQGSSLEETIASLKAEVEGFKQERQAGVS
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0; Indels
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LOCATION: (608)..(673)
OTHER INFORMATION: short form lacks nucleotides 608-673
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09862802A
Patent No. 6756478
GENERAL INFORMATION:
APPLICANT: Valladeau, Jenny
APPLICANT: Ravel, Odile
APPLICANT: Bates, Elizabeth Ester N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HWVCEAGLGOTSOESH 316
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SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 316
Matches 316; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Unknown FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 2
US-09-862-802A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241
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61 ONSKFORDLVTLRTDFSNFTSNTVAELQALTSQGSSLEETIASLKAEVEGFKQERQA--- 117
154 GTCCPVNWVEHQDSCYWFSHSGMSWAEAEKYCQLKNAHLVVINSREEQNFVQKYLGSAYT 213
                                                                 297
                                                                                                      273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 ELQEHTTQKAHLGHCPHCPSVCVPVHSEMLLRVQQLVQDLKKLTCQVATLNNN---ASTE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MTRIYENFQYLENKVKVQGFKNGPLPLQSLLQRLRSGPCHLLLSLGLGLLLLVIICVVGF 60
                                                                                     214 WMGLSDPEGAWKWVDGTDYAIGFQNWKFQQPDDWQGHGLGGGEDCAHFHPDGRWNDDVCQ
                                                                 238 WMGLSDPEGAWKWVDGTDYATGFQNWKPGQPDDWQGHGLGGGEDCAHFHPDGRWNDDVCQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 292;
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                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Advances
APPLICANT: Advances
APPLICANT: Cocks, Benjamin G.
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
NOWHER OF SEQUENCES: 5
NORBESONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1544; DB 2;
Pred. No. 4.4e-148;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF-0095-1 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/113,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/688,342
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0095.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPHONE: 415-855-4166
                                                                                                                                               298 RPYHWVCEAGLGQTSQESH 316
                                                                                                                                                                          274 RPYHWVCEAGLGQTSQESH 292
                                                                                                                                                                                                                                                                                             Sequence 4, Application US/09113788 Patent No. 5969104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 90.6%;
Matches 289; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 292 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 292 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIBRARY: GenBank
CLONE: 1235724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-113-788-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ONSKFORDLVTLRTDFSNFTSNTVAEIQALTSQGSSLEBTIASLKAEVEGFKQERQA--- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 ELQEHTTQKAHLGHCPHCPSVCVPVHSEMLLRVQQLVQDLKKLTCQVATLNNN---ASTE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----VHSEMLLRVQQLVQDLKKLTCQVATLNNNGEEASTE 153
                                             LSDPEGAWKWVDGTDYATGFQNWKPGQPDDWQGHGLGGGEDCAHFHPDGRWNDDVCQRPY 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 GTCCPVNWVEHQDSCYWFSHSGMSWAEAEKYCQLKNAHLVVINSREEQNFVQKYLGSAYT 237
    154 CPVNWVEHQDSCYWFSHSGMSWAEAEKYCQLKNAHLVVINSREEQNFVQKYLGSAYTWMG 213
                                                                 1 MTRTYENFQYLENKVKVQGFKNGPLPLQSLLQRLRSGPCHLLLSLGLGLLLLVIICVVGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MTRIYENFQYLENKVKVQGFKNGPLPLQSLLQRLRSGPCHLLLSLGLGLLLLVIICVVGF
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                                                                                                                                                                                                                                         ratent No. 5871964
; GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Gocks, Benjamin G.
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/688,342
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 9F-0095-1 CIP
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-685-0555
TELEFAX: 415-685-0555
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                          Sequence 4, Application US/08688342
Patent No. 5871964
                                                                                                                              HWVCEAGLGQTSQESH 316
                                                                                                                                                                 274 HWVCEAGLGOTSOESH 289
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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Best Local Similarity
Matches 289; Conserv
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CLONE: 1235724
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                                                                                                                                                                                                                              RESULT 4
US-08-688-342-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-688-342-4
                                                                                                                            301
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us-10-829-107-4.rai

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121 BLQEHTTQKAHLGHCPHCPSVCVPVHSEMLLRVQQLVQDLKKTTCQVATLNNN---ASTF 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135 GTCCPVNWVEHQDSCYWFSHSGMSWAEAEKYCQLKNAHLVVINSREEQNFVQKYLGSAYT 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         195 WMGLSDPEGAWKWVDGTDYATGFQNWKPGQPDDWQGHGLGGGGGDCAHFHPDGRWNDDVCQ 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178 GICCPVNWVEHQDSCYWFSHSGMSWAEAEKYCQLKNAHLVVINSREEQNFVQKYLGSAYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MTRIYENFQYLENKVKVQGFKNGPLPLQSLLQRLRSGPCHLLLSLGLGLLLLVIICVVGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MTRIYENFQYLENKVKVQGFKNGPLPLQS--------LLLLVIICVVGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

82.1%; Score 1427.5; DB 3; Length 273;
Best Local Similarity 84.6%; Pred. No. 2.6e-136;
Matches 270; Conservative 0; Mismatches 0; Indels 49;
RESULT 7

US-09-111-470-10

Sequence 10, Application US/09111470

Sequence 10, Application US/09111470

Sequence 10, 6277959

GENERAL INCORMATION:

APPLICANT: Valideau, Jenny
APPLICANT: Bates, Blizabeth E.M.

APPLICANT: Ford, John

APPLICANT: Saeland, Sem

APPLICANT: Lebecque, Serge J.E.

TITLE OF INVENTION: Related Reagents

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSE: DNAX Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/111,470

FILING DATE: 08-JUL-1998

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/053,080

FILING DATE: 09-JUL-1997

ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.

REGISTRATION NUMBER: 34,090

REFERENCE/DOCKET NUMBER: SP0695

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (650) 496-1200
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (650)852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 273 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-111-470-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/09862802A

Sequence 12, Application US/09862802A

Batent No. 6756478

GENERAL INPORMATION:
APPLICANT: Valladeau, Jenny
APPLICANT: Valladeau, Jenny
APPLICANT: Ravel, Odile
APPLICANT: Bates, Elizabeth Ester Mary
APPLICANT: Escaland, Sem
APPLICANT: Lebecque, Serge J.E.
APPLICANT: Saeland, Sem
TITLE OF INVENTION: Isolated Mammalian Membrane Protein Genes; Related Reagents
FILE REFERENCE: SF0695 B
CURRENT APPLICATION NUMBER: US/09/862,802A
CURRENT APPLICATION NUMBER: US 60/053,080
FRIOR FILING DATE: 1997-07-09
FRIOR FILING DATE: 1998-07-08
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
SEQ ID NO 12
LENGTH: 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: mammalian protein (ASGPRm is a macrophage derived ASGPR)
                                                         154 GTCCPVNWVEHQDSCYWFSHSGMSWAEAEKYCQLKNAHLVVINSREEQNFVQKYLGSAYT 213
                                                                                                                                                                                                                                            214 WMGLSDPEGAWKWVDGTDYATGFQNWKPGQPDDWQGHGLGGGEDCAHFHPDGRWNDDVCQ 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 QNSKFQRDLVTLRTDFSNFTSNTVAEIQALTSQGSSLEETIASLKAEVEGFKQERQA--- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 BLQEHTTQKAHLGHCPHCPSVCVPVHSEMLLRVQQLVQDLKKLTCQVATLNNN---ASTE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 ------VHSEMILRVQQLVQDLKKLTCQVATLNNNGEEASTE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GICCPVNWVEHQDSCYWFSHSGMSWAEAEKYCQLKNAHLVVINSREEQNFVQKYLGSAYT 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154 GTCCPVNWVEHQDSCYWPSHSGMSWAEAEKYCQLKNAHLVVINSREEQNPVQKYLGSAYT 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTCCPVNWVEHQDSCYWFSHSGMSWAEAEKYCQLKNAHLVVINSREEQNFVQKYLGSAYT 237
                                                                                                                                                                                                                   WMGLSDPEGAWKWVDGTDYATGFQNWKPGQPDDWQGHGLGGGEDCAHFHPDGRWNDDVCQ 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ONSKFORDLVTLRTDFSNFTSNTVABIQALTSQGSSLEETIASLKAEVEGFKQERQAGVS 120
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90.6%; Pred. No. 4.4e-148;
tive 0; Mismatches 0;
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Matches 289; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
US-09-862-802A-12
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60 FQNSKFQRDLVTLRTDFSNFTSNTVAEIQALTSQGSSLEETIASLKAEVEGFKQERQAGV 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 CCPVNWVEHQDSCYWFSHSGMSWAEAEKYCQLKNAHLVVINSREEQNFVQKYLGSAYTWM 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 SELQEHTTQKAHLGHCPHCPSVCVPVHSEMLLRVQQLVQDLKKLTCQVATLNNNASTEGT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 GLSDPEGAWKWVDGTDYATGFQNWKPGQPDDWQGHGLGGGEDCAHFHPDGRWNDDVCQRP 299
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                                                                                                                                                                                                                                                            SOFTWARE: FASTSEQ VERBON 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/688,342
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISSTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0095-1 CIP
TELECOMMUNICATION INFORMATION:
TELECHONE: 415-855-0555
         CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
CITY: Palo Alto
CUTY: US
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/09113788; Patent No. 5969104; GENERAL INFORMATION: APPLICANT: Au-Young, Janice; APPLICANT: Cocks, Benjamin G.; APPLICANT: Goli, Surya K.; APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  300 YHWVCEAGLGQTSQE 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           273 YRWVCETELDKASÓE 287
                                                                                                                                                                                                                    COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 291 amino acida
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO. SEQUENCE CHARACTERISTICS
  SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIBRARY: GenBank
CLONE: 179079
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US-09-113-788-5
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                                                                                                                                                                                                                                                                                 APPLICANT: Ford, John
APPLICANT: Ebecque, Serge J.E.
APPLICANT: Lebecque, Serge J.E.
APPLICANT: Saeland, Sem
TITLE OF INVENTION: Isolated Mammalian Membrane Protein Genes; Related Reagents
FILE REFERENCE: SF0695 B
CURRENT APPLICATION NUMBER: US/09/862,802A
CURRENT PILING DATE: 2001-05-22
RIOR FILING DATE: 1997-07-09
FRIOR FILING DATE: 1997-07-09
FRIOR FILING DATE: 1998-07-08
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 GTCCPVNMVEHQDSCYWFSHSGMSWAEAEKYCQLKNAHLVVINSREEONFVOKYLGSAYT 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ONSKFORDLVTLRTDFSNFTSNTVAEIQALTSQGSSLEETIASLKAEVEGFKQERQAGVS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: mammalian nucleic acid and protein
US-09-862-802A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

82.1%; Score 1427.5; DB 4
Best Local Similarity 84.6%; Pred. No. 2.6e-136;
Matches 270; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Au-Young, Janice
APPLICANT: Cocks, Benjamin G.
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Valladeau, Jenny
APPLICANT: Ravel, Odile
APPLICANT: Bates, Elizabeth Ester Mary
APPLICANT: Ford, John
APPLICANT: Lebecque, Serge J.E.
APPLICANT: Saeland, Sem
                                                                                                                                                    Sequence 10, Application US/09862802A
Patent No. 6756478
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Patent No. 5871964
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           298 RPYHWVCEAGLGQTSQESH 316
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298 RPYHWVCEAGLGQTSQESH 316
                       255 RPYHWVCEAGLGQTSQESH 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Unknown
                                                                                                        RESULT 8
US-09-862-802A-10
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US-08-688-342-5
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TOPOLOGY:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MTKEYQDLQHLDNEESDHHQLRKGPPPPQPLLQRLCSGPRLLLLSLGLSLLLLVVVVVVVIG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 53.1%; Score 923.5; DB 2; Length 291; Best Local Similarity 54.6%; Pred. No. 3.5e-85; Matches 172; Conservative 47; Mismatches 67; Indels 29
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS: 5
CORRESPONDENCE ADDRESS: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                      PF-0095-1 CIP
                                                                                                                           ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION WUMBER: US/09/113,788
FILING DATE:
                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/688,342
FILING DATE:
                                                                                                                                                                                                                                                                                                                            ATTONEY AGENT:
NAME: Billings, Lucy J.
REGISTRATION UNDRER: 36,749
REFERENCE/DOCKET NUMBER: PF-06
TELECOMMUNICATION INFORMATION:
TELEFAM: 415-85-0555
TELEFAM: 415-85-0555
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
US-09-111-470-5
; Sequence 5, Application US/09111470
; Patent No. 6277959
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300 YHWVCEAGLGQTSQE 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         273 YRWVCETELDKASOE 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 291 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
| IMMEDIATE SOURCE:
| LIBRARY: GenBank
| CLONE: 179079
| US-09-113-788-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ropology: linear
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                                                                                                   STATE: CA
                                                                                                                    COUNTRY:
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120 SELOEHTTOKAHLGHCPHCPSVCVPVHSEMLLRVQQLVQDLKXLTCQVATLNNNASTEGT 179
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APPLICANT: Rave.,
APPLICANT: Bates, Elizabe...
APPLICANT: Bates, Elizabe...
APPLICANT: Bated, John
APPLICANT: Lebecque, Serge J.E.
TITLE OF INVENTION: Related Reagents
ITLE OF INVENTION: Related Reagents
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE:
CTREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S3.1%; Score 923.5; DB 3; Length Similarity 54.6%; Pred. No. 3.5e-85; Conservative 47; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: RADABLE FORM:
MEDIUM TYPE: RADABLE FORM:
MEDIUM TYPE: RADABLE FORM:
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: DATE: DAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  not relevant
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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233 GLHDQNGPWKWVDGTDYETGFKNWRPEQPDDWYGHGLGGGGDCAHFTDDGRWNDDVCQRP 292
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                                                                                                                                                                                                                                                                                29; Gaps
                                                                                                                                                                                                                                       Length 311;
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APPLICANT: Valladeau, Jenny
APPLICANT: Ravel, Odile

APPLICANT: Ravel, Odile

APPLICANT: Ravel, Odile

APPLICANT: Ravel, Odile

APPLICANT: Saeland, Sem

APPLICANT: Saeland, Sem

APPLICANT: Lebecque, Serge J.E.

TITLE OF INVENTION: Mammalian Membrane Protein Genes;

TITLE OF INVENTION: Related Reagents

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:
ADDRESSE: DARX Research Institute
STREET: 901 California Avenue

CITY: Palo Alto

STATE: California

COUNTRY: USA
                                                                                                                                                                                                                                                                                   Indels
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ZIP: 94304-1104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/111,470
FILING DATE: 08-JUL-1998
                                                                                                                                                                                                                                                                                   67;
                                                                                                                                                                                                                                     Query Match
53.1%; Score 923.5; DB 4
Best Local Similarity 54.6%; Pred. No. 3.9e-85;
Matches 172; Conservative 47; Mismatches 67
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9962
LENGTH: 311
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/053,080
FILING DATE: 09-JUL-1997
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                             TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                         US-09-949-016-9962
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                                                                                                                                 APPLICANT: Ravel, Odile
APPLICANT: Ravel, Odile
APPLICANT: Bates, Elizabeth Ester Mary
APPLICANT: Bates, Elizabeth Ester Mary
APPLICANT: Bates, Elizabeth Ester Mary
APPLICANT: Lebecque, Serge J.E.
APPLICANT: Saeland, Sem
TITLE OF INVENTION: Isolated Mammalian Membrane Protein Genes; Related Reagents
FILE REPERENCE: SF0695 BR.
CURRENT APPLICATION NUMBER: US 60/053,080
PRIOR FILING DATE: 1997-07-09
PRIOR FILING DATE: 1998-07-09
PRIOR FILING DATE: 1998-07-08
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9962, Application US/09949016
; Sequence 9962, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REPERENCE: CL00130,
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT PILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53.1%; Score 923.5; DB 4 54.6%; Pred. No. 3.5e-85; tive 47; Mismatches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: mammalian protein US-09-862-802A-5
                                           Sequence 5, Application US/09862802A
Patent No. 6756478
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                                                                                          GENERAL INFORMATION:
APPLICANT: Valladeau, Jenny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 54.69
Matches 172; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
US-09-949-016-9962
                        US-09-862-802A-5
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179

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GENERAL INC. 8/36410;

APPLICANT: Valladeau, Jenny
APPLICANT: Valladeau, Jenny
APPLICANT: Bates, Elizabeth Ester Mary
APPLICANT: Bates, Elizabeth Ester Mary
APPLICANT: Bates, Elizabeth Ester Mary
APPLICANT: Bates, Serge J.E.
APPLICANT: Saeland, Sem
TITLE OF INVENTION: Isolated Mammalian Membrane Protein Genes; Related Reagents
TITLE OF INVENTION: 18010-05-22
FILE REFERENCE: SF0695 B
CURRENT APPLICATION NUMBER: US/09/862,802A
CURRENT FILING DATE: 2001-05-22
FRIOR FILING DATE: 1997-07-09
FRIOR FILING DATE: 1998-07-08
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
LENGTH: 287
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Matches 146; Conservative 50; Mismatches 89; Indels
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CTHER INFORMATION: mammalian protein
US-09-862-802A-6
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; Patent No. 6756478
NAME: Ching, Edwin P.
REGIZTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: SF065
TELECOMMUNICATION INPORMATION:
TELEPAX: (650)862-9196
TELEPAX: (650)496-1200
INPORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 287 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
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                                                May 27, 2005, 12:44:45 ; Search time 165 Seconds
GenCore version 5.1.6
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## ALIGNMENTS

Primate; dendritic cell membrane protein; DCMP1; DCMP2; chromosomal abnormality; expression misregulation; abnormal proliferation; regeneration; degeneration; haematopoietic cell. Saeland S, Lebecque SJE; Primate DCMP2 C-lectin family gene protein sequence Ford J, Bates EEM, AAW88125 standard; protein; 316 AA 98WO-US013436 97US-0053080P

with abnormal physiology or development.

Claim 2; Page 68-69; 82pp; English.

Dendritic cell membrane protein 1 (DCWP1) and DCMP2 nucleic acids can be used as markers for distinguishing cell types, including genomic aspects of cells, as well as mRNA and protein expression patterns. They can also be used to detect chromsomal abnormalities. The proteins can be used to dispance disorders associated with expression misregulation. They can also be used to treat conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions or degeneration and atrophy may be modulated using the proteins. The proteins may also play a role in regulation or development of manacopoletic cells

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Claim 10; Page 607-608; 672pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QNSKFQRDLVTLRTDFSNFTSNTVAEIQALTSQGSSLEETIASLKAEVEGFKQERQAGVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 QNSKPQRDLVTLRTDFSNPTSNTVAEIQALTSQGSSLEETIASLKAEVEGFKQERQAGVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELQEHTTQKAHLGHCPHCPSVCVPVHSEMLLRVQQLVQDLKKLTCQVATLNNNASTEGTC 180
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                                                                                           Length 316;
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                                                                                           100.0%; Score 1738; DB 2; 100.0%; Pred. No. 1.9e-154;
                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                 Matches 316; Conservative
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Yamazaki V, Ujwal ML,
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    Sequence 316 AA;
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treating inflammatory conditions such as arthritis, nephritis, Crohn's disease, ischaemia-reperfusion injury, shock, sepsis, immune responses and cases, ischaemia-reperfusion injury, shock, sepsis, immune responses cancer and for promoting wound healing. The sequences are used to induce the proliferation of neural cells and regeneration of nerve and brain tissue, and are useful for the treatment of central and peripheral cervous system diseases and neuropathies, such as Alzheimer's disease, Parkinson's disease, Huntington's disease and amyotrophic lateral sclerosis. The sequences are involved in chemocactic or chemokinetic activity, regulation of haematopoiesis, treatment of myeloid or lymphoid cell disorders and platelet disorders such as thrombocycopenia, regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, tissue repair, healing of burns, inclaions, ulcers, treatment of esteoporosis, osteoporation of bone, cartilage, tendon, ligament and/or nerve tissue court, tissue repair, healing of burns, inclaions, ulcers, treatment of steoporosis, osteoporation and treatment of lung or liver fibrosis, repertusion injury in various tissues, immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal influry in various tissues, immune deficiencies and mysthemia gravis, allergic conditions such as asthma, thrombolysis or thrombosis and coagulation disorders. Sequences AbG6666-AbG66758 represent human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QNSKFQRDLVTLRTDFSNFTSNTVAEIQALTSQGSSLEETIASLKAEVEGFKQERQAGVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELQEHTTQKAHLGHCPHCPSVCVPVHSEMLLRVQQLVQDLKKLTCQVATLNNN---ASTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MTRTYENFOYLENKVKVQGFKNGPLPLQSLLQRLRSGPCHLLLSLGLGLLLLVIICVVGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Gaps
invention relates to human novel polynucleotides and associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 5; Length 319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98.9%; Score 1718.5; DB 5
98.7%; Pred. No. 1.3e-152;
ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            novel polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU69170 standard; protein; 319 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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Query Match
Best Local Similarity
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                                                                                                 Sequence 319 AA;
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15-MAY-2001;
16-MAY-2001;
18-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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07-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-MAY-2001;
23-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-MAY-2001;
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                                                                                                                                                        Best Local Sim:
Matches 315;
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8888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     preferably a NOWX-associated disorder. The sequences are useful for treating, preventing or diagnosting diseases such as metabolic disorders, diabetes, obesity, infectious diseases (urlal, bacterial, fungal, helminthic, and protozoal, anorexia, cancer, cardiovascular disorders (e.g. hypertension, atherosclerosis), neurodegenerative disorders (e.g. hypertension, atherosclerosis), neurodegenerative disorders (e.g. hypertension, atherosclerosis), neurodegenerative disorders (e.g. sethman and various dyslipidemic disorders, inflammatory skin disorders, asthma and various dyslipidemias. The nucleic acids and polypeptides may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, cell differentiation, cell proliferation, haematopoiesis, wound healing and anglogenesis, and in the generation of antibodies that bind immunospecifically to NOVX substances
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to human NOVX polypeptides and the polynucleotides encoding them. The polypeptides, polynucleotides and antibodies that bind immunospecifically to the polypeptides are useful in the manufacture of a medicament for treating a syndrome associated with a human disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boldog FL, Burgess CL, Lach V, Gorman L, Gunther E, Guo X; Liu X, Malyankar UM, Miller CE; Liu X, Malyankar UM, Rieger DK, Shenoy SG; Crivalan M, Pena CEA, Rieger DK, Shenoy SG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alsobrook JP, Anderson DW, Constant V, Gc
Chapoval A, Edinger S, Gerlach V, Gc
Kekuda R, Lepley DM, Li L, Liu X, N
Millet I, Padigaru M, Patturajan M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 170; 340pp; English.
protozoal infection; hypertension
                                                                                                                                                                                                          04-MAY-2001; 2001US-0288950F.
07-MAY-2001; 2001US-0289087P.
15-MAY-2001; 2001US-0291053P.
16-MAY-2001; 2001US-0291243P.
16-MAY-2001; 2001US-0291243P.
21-MAY-2001; 2001US-0292001P.
22-MAY-2001; 2001US-0292410P.
23-MAY-2001; 2001US-029410P.
23-MAY-2001; 2001US-029410P.
31-MAY-2001; 2001US-029410P.
31-MAY-2001; 2001US-0294827P.
31-MAY-2001; 2001US-029898P.
31-MAY-2001; 2001US-032898P.
31-MAY-2001; 2001US-032898P.
31-MG-2001; 2001US-0313388P.
21-MG-2001; 2001US-0313388P.
21-MG-2001; 2001US-0313388P.
21-MG-2001; 2001US-031338P.
21-MG-2001; 2001US-031338P.
21-MG-2001; 2001US-031338P.
21-MG-2001; 2001US-031338P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-SEP-2001; 2001US-0324757P.
27-SEP-2001; 2001US-0325314P.
27-SEP-2001; 2001US-0325682P.
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                                                                            WO200290504-A2
                                       Homo sapiens,
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                                                                                                                                                                                                                                                                                                                                                                                                                      120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELQEHTTQKAHLGHCPHCPSVCVPVHSEMLLRVQQLVQDLKKLTCQVATLNNN---ASTE 177
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for use in therapeutic or diagnostic methods. The nucleic acids are further used as hybridisation probes, and in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. Sequences ABU69126-ABU69171 represent human NOVX polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MTRIYENPQYLENKVKVQGFKNGPLPLQSLLQRLCSGPCHLLLSLGLGLLLLVIICVVGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTCCPVNWVEHQDSCYWFSHSGMSWAEAEKYCQLKNAHLVVINSREEQNFVQKYLGSAYT
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                                                                                                                                                                        319;
                                                                                                                                                                        DB 6; Length
                                                                                                                                                                                                                         Indels
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                                                                                                                                                                        Score 1718.5; DB 6
Pred. No. 1.3e-152;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADO08343 standard; protein; 315
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2001US-0289087P.
2001US-0290753P.
2001US-0291189P.
2001US-02912413P.
2001US-0292011P.
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2001US-0293107P.
2001US-0294110P.
2001US-0294434P.
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                                                                                                                                                                        98.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, diabetes, atherosclerosis, asthma or AIDS, and in chromosome mapping, tissue typing or pharmacogenomics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FL, Burgess CE, Casman SJ;
Gorman L, Gunther E, Guo XS;
Malyankar UM, Miller CE;
Pena CEA, Rieger DK, Shenoy SG;
Vernet CAM, Voss EZ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alsobrook JP, Anderson DW, Boldog FL, Chapoval A, Edinger SR, Gerlach V, GG Kekuda R, Lepley DW, Li L, Liu X, Wa Millet I, Padigaru M, Patturajan M, E Shimkets RA, Spytek KA, Taupier RJ, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; SEQ ID NO 90; 219pp; English.
         31-JUL-2001; 2001US-0308901P.
17-AUG-2001; 2001US-031338B.
21-AUG-2001; 2001US-031335P.
17-SEP-2001; 2001US-0313937P.
17-SEP-2001; 2001US-0313937P.
25-SEP-2001; 2001US-0325802P.
27-SEP-2001; 2001US-0325814P.
27-SEP-2001; 2001US-0325882P.
27-NOV-2001; 2001US-0336882P.
14-DEC-2001; 2001US-0336882P.
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Chapoval, A, Edily...
Kekuda R, Lepley DM, Li L,
Millet I, Padigaru M, Patr
                                                                                                                                                                                                                                                                                                                                                  LIU X.
MALYANKAR U M.
MILLER C E.
MILLET I.
                                                                                                                                                                        ALSOBROOK J P.
ANDERSON D W.
BOLDOG F L.
BURGESS C E.
CASWAN S J.
CHAPOYAL A.
EDINGER S R.
GERLACH V.
                                                                                                                                                                                                                                                                                                                                                                                                  PADIGARU M.
PATTUBAJAN M.
PENA C E A.
RIEGER D K.
SHENOY S G.
SHENOY S G.
SYTEK R A.
TAUPIER R J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERNET C A M.
VOSS E Z.
ZERHUSEN B D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2004-122037/12.
                                                                                                                                                                                                                                                                        GORMAN L.
GUNTHER E.
GUO X S.
KEKUDA R.
LEPLEY D M.
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                                                                                                                                                                        (ALSO/)
(ANDE/)
(BOLD/)
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(SPYT/)
(TAUP/)
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(VOSS/)
(ZERH/)
                                                                                                                                                                                                            (BURG/)
(CASM/)
(CHAP/)
(GERL/)
(GORM/)
(GUOX/)
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(LEPL/)
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(MALY/)
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(PADI/)
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                                                                                                                                                                              61 QNSKFQRDLVTLRTDFSNFTSNTVAEIQALTSQGSSLEETIASLKAEVEGFKQERQAGVS 120
                                                                                                                                                                                                                                                     ELQEHTTQKAHLGHCPHCPSVCVPVHSEMLLRVQQLVQDLKKLTCQVATLNN--NASTEG 178
                                                                                                                                                                                                                                                                        119 ELQEHTTQK-HLGHCPHCPSVCVPVHSEMLLRVQQLVQDLKILTCQVATLNNGEEASTEG 177
                                                                                                                                                                                                                                                                                                                                             178 TCCPVNWVEHQDSCYWFSHSGMSWAEAEKYCQLKNAHLVVINSREEQNFVQKYLGSAYTW 237
                                                                                                                                                                                                                                                                                                                                                                                                                  238 MGLSDPEGAWKWVDCTDYATGFQNWKPGQPDDWGGHGLGGGEDCAHFHPDGRWNDDVCQR 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dendritic cell membrane protein 1 (DCMP1) and DCMP2 nucleic acids can be used as markers for distringuishing cell types, including genomic aspects of cells, as well as mRNA and protein expression patterns. They can also be used to detect chromosowal abnormalities. The proteins can be used to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dendritic cell membrane proteins - used to treat conditions associated with abnormal physiology or development.
                                                                                                                               1 MTRIYENFQYLENKVKVVQFFKNGPLPLQSLLQRLCSGPCHLLLSLGLGLLLLVITCVVGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lebecque SJE;
                                                                                                        1 MTRIYENFQYLENKVKVQGFKNGPLPLQSLLQRLRSGPCHLLLSLGLGLLLLLVIICVVGF
                                                                                                                                                                                                                                                                                                                        TCCPVNWVEHQDSCYWFSHSGMSWAEAEKYCQLKNAHLVVINSREEQNFVQKYLGSAYTW
                                                                                                                                                                                                                                                                                                                                                                                              MGLSDPEGAWKWVDGTDYATGFQNWKPGQPDDWQGHGLGGGEDCAHFHPDGRWNDDVCQR
                                                                       Gaps
                                                                     2
                                 DB 8; Length 315;
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                                                                   5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ford J, Saeland S,
                                 Score 1651.5; DB 8
Pred. No. 2.6e-146;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2(b); Page 76-78; 82pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW88129 standard; protein; 273 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             298 PYHQVCEAGKGQTSQESH 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PYHWVCEAGLGQTSQESH 316
                                   95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98WO-US013436.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-MAY-1999 (first entry)
                          Ouery Match
Best Local Similarity 96.9
Matches 308; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Valladeau J, Ravel O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SCHE ) SCHERING CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-120786/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAX04868
Sequence 315 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia.
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New isolated NOVX polypeptides and polymucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. ostecoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
                                                                                                                                                                                                                                                                                                        Anderson DW, Boldog FL, Burgess CE, Casman SJ;
dinger S, Gerlach V, Gorman L, Gunther E, Guo X;
ley DM, Li L, Liu X, Malyankar UW, Miller CE;
igaru M, Patturajan M, Pena CEA, Rieger DK, Shenc
spytek KA, Taupier RJ, Vernet CAM, Voss EZ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 169; 340pp; English.
                           2001US-0293107P.
2001US-0294130P.
2001US-0294434P.
2001US-0294827P.
2001US-0298988P.
2001US-0398981P.
                                                                                                                                                           2001US-0322802P.
2001US-0324757P.
2001US-0325314P.
2001US-0325682P.
                                                                                                                      2001US-0313851P.
2001US-0313937P.
2001US-0322701P.
                                                                                                                                                                                                                21-NOV-2001; 2001US-0332129P.
03-DEC-2001; 2001US-0336882P.
14-DEC-2001; 2001US-0340305P.
01-MAY-2002; 2002US-00138588.
                                                                                                                                                                                                                                                                                                                         Chapoval A, Edinger S, G
Kekuda R, Lepley DM, Li
Millet I, Padigaru M, Pa
Shimkets RA, Spytek KA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 89.5
Matches 263; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      asthma, or infections.
                                                                                                                                                                                                                                                                                   (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-103512/09.
                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ACA10154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 267 AA;
                                                                               18-JUN-2001;
31-JUL-2001;
17-AUG-2001;
                                                                                                                                                                                                                                                                                                              Alsobrook JP,
                                                                     31-MAY-2001;
                                                                                                                       21-AUG-2001;
                                                                                                                                    21-AUG-2001;
17-SEP-2001;
                                                                                                                                                              17-SEP-2001;
                                                                                                                                                                           25-SEP-2001;
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                                                      30-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                               Zerhusen BD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23
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                                                                                                                                                                                                                                                                                                                                                                                  GTCCPVNWVEHQDSCYWFSHSGMSWAEAEKYCQLKNAHLVVINSREEQNFVQKYLGSAYT 194
                                                                                                                                                                                                                                                                                                                                                                                                                       WMGLSDPEGAWKWVDGTDYATGFONWKPGQPDDWQGHGLGGGEDCAHFHPDGRWNDDVCQ 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; NOVX; metabolic disorder; diabetes; infectious disease; obesity; anorexia; cancer; cardiovascular disorder; asthma; neurogenesis; neurodegenerative disorder; epilepsy; immune disorder; osteoarthritis; haematopoietic disorder; inflammatory skin disorder; dyslipidemia; haematopoiesis; wound healing; anglogenesis; bacterial infection; viral infection; tungal infection; helminthic infection; atherosclerosis;
diagnose disorders associated with expression misregulation. They can also be used to treat conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions or degenerative conditions. Abnormal proliferation, regeneration, degeneration and atrophy may be modulated using the proteins. The proceins may also play a role in regulation or development of haematopoietic cells
                                                                                                                                                                                                                                                         QNSKPQRDLVTLRTDFSNFTSNTVAEIQALTSQGSSLEETIASLKAEVEGFKQERQAGVS 120
                                                                                                                                                                                                                                                                                                            121 ELQEHTTQKAHLGHCPHCPSVCVPVHSEMLLRVQQLVQDLKKLTCQVATLNNN---ASTE 177
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                                                                                                                                                                                                                                                                        QNSKFQRDLVTLRTDFSNFTSNTVAEIQALTSQGSSLEETIASLKAEVEGFKQERQA---
                                                                                                                                                                                                                             1 MTRIYENFOYLENKVKVQGFKNGPLPLQS-----------LLLLVIICVVGF
                                                                                                                                                                                                     MTRTYENFOYLENKVKVQGFKNGPLPLQSLLORLRSGPCHLLLSLGLGLLLLVIICVVGF
                                                                                                                                                                            Gaps
                                                                                                                                                                         49;
                                                                                                                                                  DB 2; Length 273;
                                                                                                                                                                           Indels
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                                                                                                                                               Score 1427.5; DB 2
Pred. No. 2.4e-125;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protozoal infection; hypertension
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPYHWVCEAGLGQTSQESH 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-MAY-2001; 2001US-0288395P.
04-MAY-2001; 2001US-028900P.
07-MAY-2001; 2001US-0289087P.
14-MAY-2001; 2001US-0290753P.
15-MAY-2001; 2001US-0291189P.
16-MAY-2001; 2001US-0291243P.
18-MAY-2001; 2001US-029201P.
21-MAY-2001; 2001US-0292374P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RPYHWVCEAGLGOTSOESH
                                                                                                                                                  82.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human NOVX polypeptide #44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                             Query Match
Best Local Similarity 84.6
Matches 270; Conservative
                                                                                                                       Sequence 273 AA;
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Shenoy SG;

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The invention relates to human NOVX polypeptides and the polynucleotides encoding them. The polypeptides, polynucleotides and antibodies that bind encoding them. The polypeptides are useful in the manufacture of a medicament for treating a syndrome associated with a human disease, confidence associated with a human disease, preferably a NOVX-associated disorder. The sequences are useful for treating, preventing or diagnosing diseases such as metabolic disorders, clabetes, obesity, infectious diseases (viral, bacterial, fungal, chalminthic, and protozoal), anorexia, cancer, cardiovascular disorders (e.g. hypertension, atherosclerosis), neurodegenerative disorders (e.g. hypertension, atherosclerosis), neurodegenerative disorders (c.g. disease, Parkinson's disease), epilepsy, immune disorders, asthma and various dyslipidemias. The nucleic acids and polypeptides may also used as targets for the identification of small molecules that module conflectation, haematopoiesis, wound healing and angiogenesis, and in the proliferation, haematopoiesis, wound healing and angiogenesis, and in the correct or disagnostic methods. The nucleic caids are further used as hybridisation probes, and in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. Sequences ABU69126-CABU69171 represent human NOVX polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TVAEIQALTSQGSSLEETIASLKAEVEGFKQERQAGVSELQEHTTQKAHLGHCPFCVC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81.2%; Score 1410.5; DB 6; Length 267; 89.5%; Pred. No. 9.1e-124; ive 0; Mismatches 4; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TVAEIQALTSQGSSLEETIASLKAEVEGFKOERQA-
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us-10-829-107-4.rag

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The invention relates to human NOVX polypeptides and the polynucleotides encoding them. The polypeptides, polynucleotides and antibodies that bind immunospecifically to the polypeptides are useful in diagnosing, treating or preventing NOVX-associated disorders such as cardiomyopathy, atherosclerosis, hypertension, scleroderma, obesity, cancer, diabetes, multiple sclerosis, infections, anorexia, cancer-associated cachexia, neurodegenerative disorders (e.g. Alzheimer's disease or Parkinson's disease), haematopoietic disorders and wasting disorders. The polynucleotides are also used as hybridisation probes, in chromosome mapping and in tissue typing. The polypeptides are also useful as vaccines. This sequence represents a human NOVX polypeptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                             New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, diabetes, atherosclerosis, asthma or AIDS, and in chromosome mapping, tissue typing or pharmacogenomics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83 TVABIQALTSQGSSLBETIASLKAEVEGFKQERQAGVSELQEHTTQKAHLGHCPRVC 142
                                                                                                                                                                                                                                                                                                                                                  Shenoy SG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GPLPLOSLLORLCSGPCHLLLSLGLGFLLLVIICVVGFQNSKFQRDLVTLRTDFSNFTSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96 --VHSEMLLRVQQLVQDLKKLTCQVATLNNNASTEGTCCPVNWVEHQDSCYWFSHSGMSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203 AEAEKYCQLKMAHLVVINSREEQNFVQKYLGSAYTWMGLSDPEGAWKWVDGTDYATGFQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 VPVHSEMLLRVQQLVQDLKKLTCQVATLNNNASTEGTCCPVNWVEHQDSCYWFSHSGMSW
                                                                                                                                                                                                                                                                                                        Gunther E, Guo XS;
UM, willer CE;
Rieger DK, Shenoy S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 TVAEIQALTSQGSSLEETIASLKAEVEGFKQERQA-----
                                                                                                                                                                                                                                                                                                        Alsobrook JP, Anderson DW, Boldog FL, Burgess CE, Chapoval A, Edinger SR, Gerlach V, Gorman L, Gun Kekuda R, Lepley DM, Li L, Liu X, Malyankar UM, Millet I, Padigaru M, Patturajan M, Pena CEA, Ri, Shimkets RA, Spytek KA, Taupier RJ, Vernet CAM, Zerhusen BD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.2%; Score 1410.5; DB 8
89.5%; Pred. No. 9.1e-124;
ive 0; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 89.57
....has 263; Conservative
                                                                                                                                                                  PENA C E A.
RIEGER D K.
SHENOY S G.
SHIMKETS R A.
SPYTEK K A.
TAUPIER R J.
                                                                                                           MILLER C E.
MILLET I.
PADIGARU M.
PATTURAJAN M.
                                                                                              MALYANKAR U M.
                                                                                                                                                                                                                                                   VERNET C A M.
VOSS E Z.
                                                                                                                                                                                                                                                                               ZERHUSEN B D
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                                     KEKUDA R.
LEPLEY D M.
GORMAN L.
GUNTHER E.
             GUNTHER E
GUO X S.
KEKUDA R.
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(LILL/)
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              202
                                        153
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                                                                                              213
                                                                                                                                                                                                                                                                                                                                    Human; NOVX; cardiomyopathy; atherosclerosis; hypertension; scleroderma; obesity; cancer; diabetes; hamophilia; graft-versus-host disease; AIDS; asthma; Crohn's disease; multiple sclerosis; infection; anorexia; cancer-associated cachexia; neurodegenerative disorder;
                           --VHSEMILIRVQQLVQDLKKITCQVATINNNASTEGTCCPVNWVEHQDSCYWFSHSGMSW
                                                                                  154 AEAEKYCQLKNAHLVVINSREEQNFVQKYLGSAYT#MGLSDPEGAWKWVDGTDYATGPQN
             143 VPVHSEMILLRVQQLVQDLKKLTCQVATLNNNASTEGTCCPVNWVEHQDSCYWFSHSGMSW
                                                                  AEAEKYCQLKNAHLVVINSREEQNFVQKYLGSAYTWMGLSDPEGAWKWVDGTDYATGFQN
                                                                                                                          WKPGQPDDWQGHGLGGGEDCAHFHPDGRWNDDVCQRPYHWVCEAGLGQTSQESH 316
                                                                                                                                      214 WKPDQPDDWQGHGLGGGEDCAHFHPVGRWNDDVCQRPYHWVCEAGLGQTSQESH 267
                                                                                                                                                                                                                                                                                                                                                                                         Alzheimer's disease; Parkinson's disease; haematopoietic disorder;
                                                                                                                                                                                                                         ADO08341 standard; protein; 267 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-MAY-2001; 2001US-0288395P.
04-MAY-2001; 2001US-0288900P.
07-MAY-2001; 2001US-028900BP.
14-MAY-2001; 2001US-029108PP.
15-MAY-2001; 2001US-0291189P.
16-MAY-2001; 2001US-0291243P.
18-MAY-2001; 2001US-0291243P.
21-MAY-2001; 2001US-029258PP.
23-MAY-2001; 2001US-029110P.
23-MAY-2001; 2001US-029410P.
23-MAY-2001; 2001US-029410P.
31-MAY-2001; 2001US-0294134P.
31-MAY-2001; 2001US-039483P.
31-MAY-2001; 2001US-0308901P.
31-MG-2001; 2001US-031338BP.
21-MG-2001; 2001US-031338BP.
21-MG-2001; 2001US-0313337P.
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25-SEP-2001; 2001US-0324757P.
27-SEP-2001; 2001US-0325314P.
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2001US-0336882P.
2001US-0340305P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001US-0325682P
                                                                                                                                                                                                                                                                                                          Human NOVX polypeptide #44.
                                                                                                                                                                                                                                                                              01-JUL-2004 (first entry)
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BOLDOG F L.
BURGESS C E.
CASMAN S J.
CHAPOVAL A.
EDINGER S R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALSOBROOK J P
                                                                                                                                                                                                                                                                                                                                                                                                        wasting disorder.
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03-DEC-2001;
14-DEC-2001;
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                                                                                                                         263
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(ANDE/)
(BOLD/)
(BURG/)
(CASM/)
(CHAP/)
(EDIN/)
(GERL/)
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29; Gaps

Indels

Pred. No. 6.3e-78; 47; Mismatches

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240 GLSDPEGAWKWVDGTDYATGFQNWKPGQPDDWQGHGLGGGEDCAHFHPDGRWNDDVCQRP 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                GLHDONGPWKWVDGTDYQTGFKNWRPEQPDDWYGHGLGGGEDCAHFTDDGRWNDDVCQRP 272
                                                                                                                                                         60 FONSKFORDLVTLRTDFSNFTSNTVAELOALTSQGSSLEETIASLKAEVEGFKQERQAGV 119
                                                                                                                                                                                1 MTRIYENFQYLENKVK-VQGFKNGPLPLQSLLQRLRSGPCHLLLSLGLGLLLLVIICVVG
                                                                                                                                                                                                                                             120 SELQEHTTQKAHLGHCPHCPSVCVPVHSEMLLRVQQLVQDLKKLTCQVATLNNNASTEGT
                                                                                                                                                                                                                                                                                                                                 180 CCPVNWVEHQDSCYWFSHSGMSWAEAEKYCQLKNAHLVVINSREEQNFVQKYLGSAYTWM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABM82572 standard; protein; 319 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-SEP-2002; 2002US-0410259P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300 YHWVCEAGLGQTSQE 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YRWVCETELDKASQE 287
  54.6%;
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                           Conservative
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Lagace RE, Sp.
Y, Kwong M, Po.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-329368/30.
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Best Local Similarity
Matches 172, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ACN41224
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    AEAEKYCQLKNAHLVVINSREEQNFVQKYLGSAYTWMGLSDPEGAWKWVDGTDYATGFQN 213
                                                                                                                                                                                                                                                                                                                                                                            Asialoglycoprotein receptor H1; AGPR; autoimmune hepatitis; autoantibody;
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s, useful
                                               WKPGQPDDWQGHGLGGGEDCAHFHPDGRWNDDVCQRPYHWVCEAGLGQTSQESH 316
                                                                          Asialo:glyco:protein receptor H1 and L-H2 soluble derivatives - c
extracellular domains, optionally also with cytoplasmic domains,
for autoimmune hepatitis diagnosis.
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/label= Extracellular_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43. .59
/label= Transmembrane_domain
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/label= Cytoplasmic_domain
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                                                                                                                                                                                                  AAW15245 standard; protein; 291
                                                                                                                                                                                                                                                                                                                                   Asialoglycoprotein receptor H1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                     diagnosis
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                                                                                                                                                     RESULT 8
AAW15245
AAW1624
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Gietzen D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F; Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV; Mooney EM, Delegeane AM, Penesar IS, Banville SC, Reddy TP; Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH; Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL; Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES; Xu X, X, wong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietze Patury S, Shi X, Suarez CJ;
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selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine autoimune/filfalmmatory disorder, developmental disorder, endocrine disorder, neurological disorder, developmental disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals molecules may also be used in genetic mapping, in identifying individuals promorphisms, as molecular weight markers, and for somatic or germline polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represents a dithp protein of the gene therapy. The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FQNSKFQRDLVTLRTDFSNFTSNTVAEIQALTSQGSSLEETIASLKAEVEGFKQERQAGV 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                     61 SQNSQLQEELRGLRETFSNFTASTEAQVKGLSTQCGNVGRKMKSLESQLE--KQQK---
                                                                                                                                                                                                                                                                                                                                                                                                               1 MTRIYENFOYLENKVK-VQGFKNGPLPLQSLLQRLRSGPCHLLLSLGLGLLLLVIICVVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 SELQEHTTOKAHLGHCPHCPSVCVPVHSEMLLRVQQLVQDLKKLTCQVATLNNN-----
                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                               55;
                                                                                                                                                                                                                                                                                                                                     52.3%; Score 908.5; DB 8; Length 319; 50.0%; Pred. No. 1.9e-76; ive 49; Mismatches 67; Indels 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   273 GHGLGGGEDCAHFHPDGRWNDDVCQRPYHWVCEAGLGQTSQE 314
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12-SEP-2002; 2002US-0410260P,
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Matches 171; Conservative
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                                                                                                                                                                                                                                                                                                    Sequence 319 AA;
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polynucleotide of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine austorial and insorders, or autolimune/fillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanchillammanch
horne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
EM, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
a CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
a RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
S, Shi X, Suarez CJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       213 NAHLVVINSREEQNFVQKYLGSAYTWMGLSDPEGAWKWVDGTDYATGFQNWKPGQPDDWQ 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to novel diagnostic and therapeutic polynucleotides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MIRTYENFOYLENKVK-VQGFKNGPLPLQSLLQRLRSGPCHLLLSLGLGLLLLVIICVVG
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tes 171; Conserv
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             Harthshorne TA,
                                                                                          Stevens KA,
Peralta CH,
                                                                                                                                                                                 Lagace RE,
                                                      Mooney EM,
                                                                                                                                                                                                                                                                                Patury S,
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ABM82573
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153 CCPVNWVEHERSCYWFSRSGKAWADADNYCRLEDAHLVVVTSWEEQVRTRRVWEAGWPRR 212

213 DHHPPSLSQKFVQHIIGPVNTWMGLHDQNGPWKWVDGTDYETGFKNWRPEQPDDWYGHGL -----QNFVQKYLGSAYTWMGLSDPEGAWKWVDGTDYATGFQNWKPGQPDDWQGHGL

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ABM82575 standard; protein; 314

ABM8257

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The invention relates to novel diagnostic and therapeutic polymucleotides selected from one of the 2722 sequences defined in the specification. A colymucleotide of the invention may have a use in gene therapy. The human colymucleotides (dithp) or polymepaper. The human changes and therapeutic polymucleotides (dithp) or polymeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules. e.g. cell proliferative disorders, endorine autoimmune/inflammatory disorder, gastrointestinal disorder, or disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungior parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide colymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represente a dithp protein of the cinvention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                              Wright RJ; Bruns CM, Marjanovic MM, Shen F;
17A, Suchorolski MT, Altus CM, Pitts SJ, Blder LV;
Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Shi X, Suarez CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
                                                                   gene therapy, human diagnostic and therapeutic polynucleotide; dithp
                          Human diagnostic and therapeutic pprotein SEQ ID NO:2822.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from WIPO at www.wipo.int/pct/en/sequences/listing.htm
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                                                                                                                                                                                                                                                                          12-SEP-2002; 2002US-0410259P.
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S. Shi X,
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                                                                                                                                                  WO2004023973-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene mapping
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Stevens KA,
Peralta CH,
                                                                                                             Homo sapiens
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Best Local Si
Matches 172,
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gene therapy; human diagnostic and therapeutic polynucleotide; dithp.

WO2004023973-A2 Ното варіепв.

12-SEP-2002; 2002US-0410259P. 12-SEP-2003; 2003WO-US028227

(INCY-) INCYTE CORP.

Human diagnostic and therapeutic pprotein SEQ ID NO:2824.

(first entry)

18-NOV-2004 ABM82575;

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The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A puricleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine autoimmune/inflammatory disorder, developmental disorders, or autoimmune/inflammatory disorder, developmental disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp conflections caused by virus, bacteria, fungi or parasite. The dithp inflections caused by virus, bacteria, fungi or parasite. The dithp conflection and also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represents a dithp protein of the gene therapy. The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/llsting.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gietzen D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kirton ES;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F; Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV; Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP; Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin E Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL; Ligadec RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gie Patury S, Shi X, Suarez CJ;
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N-PSDB; ACN41227.
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FONSKFORDLVTLRTDFSNFTSNTVAEIQALTSQGSSLEETIASLKAEVEGFKQERQAGV 119
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Local Similarity 50.9 les 172; Conservative

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Claim 27; Page; 190pp; English
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                                                                                                                                                                                                                                                                 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
Patury S, Shi X, Suarez CJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosting a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping.
                                                                             1 MTKEYQDLQHLDNEESDHHQLRKGPPPPQPLLQRLCSGPRLLLLLSLGLSLLLLVVVCVIG
                                                                                                                                                                                                             120 SELQEHTTQKAHLGHCPHCPSVCVPVHSEMLLRVQQLVQDLKKLTCQVATLNNNASTEGT
                                                                                                                                                                           115 -DLSED-------GSLLLHVKOFVSDLRSLSCOMAALOGNGS-ERT
                                                                                                                                                                                                 180 CCPVNWVEHQDSCYWFSHSGMSWAEAEKYCQLKNAHLVVINSREE-------
                                                                                                                                                                                                                                           -----QNFVQKYLGSAYTWMGLSDPEGAWKWVDGTDYATGFQNWKPGQPDDWQGHGL
                                                                                                                                                                                                                                                         213 DHHPPSLSQKFVQHHIGPVNTWMGLHDONGPWKWVDGTDYETGFKNWRPEOPDDWYGHGL
                                                                1 MTRIYENFOYLENKVK-VOGFKNGPLPLOSLLORLRSGPCHLLLSLGLLLLLVIICVVG
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
                                          52;
                      Length 314;
                    51.9%; Score 902; DB 8; Length 31
50.9%; Pred. No. 7.4e-76;
ive 47; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   Human diagnostic and therapeutic pprotein SEQ ID NO:2820.
                                                                                                                                                                                                                                                                                                     273 GGGEDCAHFTDDGRWNDDVCQRPYRWVCETELDKASQE 310
                                                                                                                                                                                                                                                                                       GGGEDCAHFHPDGRWNDDVCQRPYHWVCEAGLGQTSQE 314
                                                                                                                                                                                                                                                                                                                                                                  ABM82571 standard; protein; 290 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-SEP-2003; 2003WO-US028227
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                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                           Matches 172; Conservative
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                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-329368/
N-PSDB; ACN41223
Sequence 314 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2004023973-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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Patury S,
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The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, or autoimmune/inflammatory disorder, developmental disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp inflammatory also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline polymorphisms, as molecular weight markers, and for somatic or germline invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 FONSKFORDLVTLRTDFSNFTSNTVAEIQALTSQGSSLEETIASLKAEVEGFKQERQAGV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 SELQEHTTQKAHLGHCPHCPSVCVPVHSEMLLRVQQLVQDLKKLTCQVATLNNNASTEGT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      189 DHHPPSLSQKFVQHHIGPVWTWMGLHDQNGPWKWVDGTDXETGFKNWRPEQPDDWYGHG 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 CCPVNWVEHERSCYWFSRSGKAWADADNYCRLEDAHLVVVTSWEEOVRTRRVWEAGWPRR 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene therapy; human diagnostic and therapeutic polynucleotide; dithp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49.6%; Score 862; DB 8; Length 290; 48.5%; Pred. No. 3.8e-72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human diagnostic and therapeutic pprotein SEQ ID NO:2819.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 CCPVNWVEHQDSCYWFSHSGMSWAEAEKYCOLKNAHLVVINSREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                249 GGGEDCAHFIDDGRWNDDVCQRPYRWVCETELDKASQE 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   277 GGGEDCAHFHPDGRWNDDVCQRPYHWVCEAGLGQTSQE 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 SONSOLQEELRGLRETPSNFTASTEAQVKGLSTQD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ŕ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-SEP-2002; 2002US-0410259P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 164; Conservative
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us-10-829-107-4.rag

AAW15250;

Gietzen D;

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The invention relates to novel diagnostic and therapeutic polymucleotides selected from one of the 2722 sequences defined in the specification. A polymucleotide of the invention may have a use in gene therappy. The human diagnostic and therapeutic polymucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine disorder, neurological disorder, gastrolitestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gent therapy. The present sequence represents a dithp protein of the invention. Note: The sequence data for this parent is not represented in the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                          New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
                                       Wright RJ, Bruns CM, Marjanovic MM, Shen F;
TA, Suchorolski MT, Altus CM, Pitts SJ, Elder IV;
Delegeane AM, Panesar IS, Banville SC, Reddy TP,
Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES,
MY, Suarez CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from WIPO at www.wipo.int/pct/en/sequences/listing.htm
                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 27; Page; 190pp; English.
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(INCY-) INCYTE CORP.
                                                                                                                                                                        Kwong M, P
S, Shi X,
                                                                                                                                                                                                                                                                  N-PSDB; ACN41222
                                                                                                                                                                                                                                                                                                                                                                                 gene mapping
                                                                                     Mooney EM, I
Stevens KA,
Peralta CH,
                                                                Harthshorne
                                              Schmidt JP,
                                                                                                                                                      Lagace RE,
Xu Y, Kwo
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120 SELQEHTTQKAHLGHCPHCPSVCVPVHSEMLLRVQQLVQDLKKLTCQVATLNNNASTEGT 179 60 FONSKFORDLVTLRTDFSNFTSNTVAEIQALTSQGSSLEETIASLKAEVEGFKQERQAGV 119 1 MIKEYQDLQHLDNEESDHHQLRKGPPPQPILQRLCSGPRILLLSLGLSLILLLVVVCVIG 60 1 MTRIYENFQYLENKVK-VQGFKNGPLPLQSLLQRLRSGPCHLLLSLGLGLLLLVIICVVG 59 -----QNFVQKYLGSAYTWMGLSDPEGAWKWVDGTDYATGFQNWKPGQPDDWQGHGL DHHPPSLSQKFVQHHIGPVNTWMGLHDQNGPWKWVDGTDYETGFKNWRPEQPDDWYGHGL CCPVNWVEHQDSCYWFSHSGMSWAEAEKYCQLKNAHLVVINSREE-----49.6%; Score 862; DB 8; Length 290; 48.5%; Pred. No. 3.8e-72; tive 37; Mismatches 61; Indels ' SONSOLOEELRGIRETFSNFTASTEAQVKGLSTQD------GGGEDCAHFTDDGRWNDDVCQRPYRWVCETELDXASQE 286 GGGEDCAHFHPDGRWNDDVCQRPYHWVCEAGLGQTSQE 314 Matches 164; Conservative Similarity Seguence 290 AA; 180 225 277 249 Query Match Best Local 9 96 硆 g 유 셤 ò ઠે 8 ઠ 셤 ò ઠે

SELQEHTTQKAHLGHCPHCPSVCVPVHSEMLLRVQQLVQDLKKLTCQVATLNNNASTEGT 179

8

AAW15250 standard; protein; 274 AA.

RESULT 15 AAW15250 ID AAW1 XX

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This polypeptide sequence comprises the cytoplasmic (CTD) and extracellular (ECD) domains of human full-length asialoglycoprotein extracellular (ECD) domains of human full-length asialoglycoprotein creeptor (AGEP) HI (See AAM15245). It can be produced on a large scale, in a form free of contaminating liver antigens, by PCR amplification (see AAM16962-65) of CTD+ECD DNA (see also AAM166950), and expression in becterial (pref. E. coll) or animal (pref. mammalian) host cells. The ECD alone (AAM15249) and AGPR L-H2 derivatives (see AAM15251-52) are also claimed. The appearance of autoantibodies against AGPR can be used as an indicator for autoimmune hepatitis (AIH), a disease that can lead to cirrhosis and fatal intractable hepatitis. Recombinant soluble AGPR crivatives can be used in a claimed method for detecting and measuring anti-AGPR antibodies, e.g. by ELISA, Western blotting, etc. This allows AIH to be diagnosed and distinguished from other diseases. AGPR and purification of asialoglycoproteins and to develop inhibiting agents against asialoglycoproteins and to develop inhibiting agents invasion, into liver cells. (Updated on 17-OCT-2003 to standardise OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FONSKFORDLVTLRTDFSNFTSNTVAEIQALTSQGSSLEETIASLKAEVEGFKQERQAGV 119
                                                                                                            Asialoglycoprotein receptor H1; AGPR; autoimmune hepatitis; autoantibody; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              extracellular domains, optionally also with cytoplasmic domains, useful for autoimmune hepatitis diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MIRIYENFQYLENKVK-VQGFKNGPLPLQSLLQRLRSGPCHLLLSLGLGLLLLVIICVVG
                                                                               Asialoglycoprotein receptor H1 cytoplasmic+extracellular domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MTKEYODLOHLDNEESDHHQLRKGPPPPOPLLORLCSGP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 274;
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50.2%; Pred. No. 6.3e-70;
iive 46; Mismatches 65
                                                                                                                                                                                                                                                               43. .274
/label= Extracellular_domain

    .42
    /label= Cytoplasmic domain

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                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                               96EP-00113349
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                                              (first entry)
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Best Local Similarity 50.21
Matches 158; Conservative
                              (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                21-AUG-1995;
                             17-OCT-2003
23-NOV-1997
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                                                                                                                                                                             Chimeric
                                                                                                                                                                                                                               Domain
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셤
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